



## HUMAN TELOMERASE

|   |     |
|---|-----|
| ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAG  | 60  |
| MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu  | 20  |
| GTGCTGCCGCTGGCCACGTTTCGTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAG | 120 |
| ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln  | 40  |
| CGCGGGGACCCGGCGGCTTTCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGG   | 180 |
| ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp  | 60  |
| GACGCACGGCCGCCCCCGCGCCCCCTCCTTCGCCAGGTGTCCTGCCTGAAGGAGCTG     | 240 |
| AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu  | 80  |
| GTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGGCGGAAGACGTGCTGGCCTTCGGC   | 300 |
| ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly  | 100 |
| TTCGCGCTGCTGGACGGGGCCCGCGGGGGCCCCCGAGGCCTTCACCACCAGCGTGCGC    | 360 |
| PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg  | 120 |
| AGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTG  | 420 |
| SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu  | 140 |
| TTGCGCCGCGTGGGCGACGACGTGCTGGTTACCTGCTGGCACGCTGCGCGCTCTTTGTG   | 480 |
| LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal  | 160 |
| CTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCCGCTGTACCAGCTCGGCGCT    | 540 |
| LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla  | 180 |
| GCCACTCAGGCCCGGCCCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAA  | 600 |
| AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu  | 200 |
| CGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGT   | 660 |
| ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly  | 220 |
| GCGAGGAGGCGGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCCAAGAGGCCAGGCGT      | 720 |
| AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg  | 240 |

*Fig. 1A*



GGCGCTGCCCCTGAGCCGAGCGGACGCCCGTTGGGCAGGGGTCTGGGCCCACCCGGGC 780  
GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly 260

AGGACGCGTGGACCGAGTGACCGTGGTTTCTGTGTGGTGTACCTGCCAGACCCGCCGAA 840  
ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu 280

GAAGCCACCTCTTTGGAGGGTGGCGTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGC 900  
GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300

CGCCAGCACCACGCGGGCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCCT 960  
ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro 320

TGTCCCCCGGTGTACGCGGAGACCAAGCACTTCTCTACTCCTCAGGCGACAAGGAGCAG 1020  
CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln 340

CTGCGGCCCTCCTTCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTC 1080  
LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360

GTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGAGGTTGCCC 1140  
ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro 380

CGCCTGCCCCAGCGCTACTGGCAAATGCGGCCCTGTTTCTGGAGCTGCTTGGGAACCAC 1200  
ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis 400

GCGCAGTGGCCCTACGGGGTGCTCCTCAAGACGCACTGCCGCTGCGAGCTGCGGTCACC 1260  
AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr 420

CCAGCAGCCGGTGTCTGTGCCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCCGAGGAG 1320  
ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu 440

GAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAG 1380  
GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln 460

GTGTACGGCTTCGTGCGGGCCTGCCTGCGCCGGCTGGTGGCCCCAGGCCTCTGGGGCTCC 1440  
ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer 480

AGGCACAACGAACGCCGCTTCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCAT 1500  
ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis 500

*Fig. 1B*



CCAAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGGCTGCGCTTGGCTG 1560  
AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu 520

CGCAGGAGCCCAGGGGTTGGCTGTGTTCGGCCGCAGAGCACCGTCTGCGTGAGGAGATC 1620  
ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle 540

CTGGCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTGCTCGAGCTGCTCAGGTCTTTC 1680  
LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe 560

TTTTATGTACGGAGACCAGTTCCTTTCAAAGAAGAGGCTCTTTTCTACCGAAGAGTGTC 1740  
PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580

TGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCACTGCGGGAG 1800  
TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu 600

CTGTCCGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGA 1860  
LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 620

CTCCGCTTCATCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTGCTG 1920  
LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 640

GGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCA 1980  
GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla 660

CTGTTACGCTGCTCAACTACGAGCGGGCGCGCGCCCCGGCCTCCTGGGCGCCTCTGTG 2040  
LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 680

CTGGGCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCAG 2100  
LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln 700

GACCCGCCGCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATC 2160  
AspProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle 720

CCCCAGGACAGGCTCACGGAGGTCATGCCAGCATCATCAAACCCAGAACACGTACTION 2220  
ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys 740

GTGCGTCGGTATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCCTCAAG 2280  
ValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys 760

*Fig. 1C*



AGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTG 2340  
SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 780

CAGGAGACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAG 2400  
GlnGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeuAsnGlu 800

GCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATC 2460  
AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle 820

AGGGGCAAGTCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTG 2520  
ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840

CTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGAC 2580  
LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp 860

GGGCTGCTCCTGCGTTTGGTGGATGATTTCTTGTGGTGACACCTCACCTCACCCACGCG 2640  
GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880

AAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACCTTG 2700  
LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu 900

CGGAAGACAGTGGTGAACCTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTT 2760  
ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 920

CAGATGCCGGCCCCACGGCCTATTCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTG 2820  
GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeu 940

GAGGTGCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTC 2880  
GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960

AACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTG 2940  
AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu 980

AAGTGTACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAAC 3000  
LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000

ATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGTCCCA 3060  
IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020

Fig. 1D



TTTCATCAGCAAGTTTGAAGAACCCACATTTTCTGCGCGTCATCTCTGACACGGCC 3120  
PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAls 1040

TCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGC 3180  
SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly 1060

GCCGCCGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCTGCTC 3240  
AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu 1080

AAGCTGACTCGACACCGTGTACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAG 3300  
LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100

ACGCAGCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGAGCCAAC 3360  
ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAlaAsn 1120

CCGGCACTGCCCTCAGACTTCAAGACCATCCTGGACTgatggccacccgcccacagccag 3420  
ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132

Gccgagagcagacaccagcagccctgtcacgccgggctctacgtcccagggaggaggagg 3480  
Cggccacacccaggcccgaccgctgggagctctgaggcctgagtgagtgtttggccgag 3540  
gcctgcatgtccggctgaaggctgagtgtccggctgaggcctgagcgagtgtccagccaa 3600  
gggctgagtgtccagcacacctgccgtcttcactccccacaggctggcgctcggtcca 3660  
ccccagggccagcttttcctcaccaggagcccggttccactccccacataggaatagtc 3720  
catccccagattcgccattgttcacccctcgccctgccctcctttgccttccacccccac 3780  
catccaggtggagaccctgagaaggaccctgggagctctgggaatttgagtgaccaaag 3840  
gtgtgccctgtacacaggcgaggaccctgcacctggatgggggtccctgtgggtcaaat 3900  
ggggggagggtgctgtgggagtaaaatactgaatatatgagttttcagttttgaaaaaaa 3960  
aaaa 3964

*Fig. 1E*



Euplotes 1 -----MEVDVDNQADNHGIHSALKTCEEIKEAKTLYSWIQKVIRCR--NQSQSHYKDLEDIA  
HT1 1 RRLGPQGWRLVQRGDPAAFRALVAQCLVCVPWDAR-PPPAAPSFQVSCLELVARVLQRLCERGAKNVLAFGFALLDGA  
EST2 1 -----MKILFEFIQDKLDID--LQTNSTYKENLKCG

Euplotes 56 IFAQTNIVATPRDYNEEDFKVIARK-----EVFSTGLMIELIDKCLVELLSSSDVSDRQKLQCFGFQKGNQ-LAK  
HT1 80 RGGPPEAFTTSVRSYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAY---QVCGPPLYQLGAATQA  
EST2 30 HFNGLDEILTT-CFALPNSRKIALP-----CLPGDLSHKAVIDHCIIYLLTGELYNN---VLTFGYKIARNEDVNN

Euplotes 126 THLLTALSTQKQYFFQDEWVQVRAMIGNELFRHLYTKYLIFQRTSEGLVQFCGNNVFDHLKVNDKFDKKQKGGAAADMNE  
HT1 157 RPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAGARRRGGASRSLPLPKRPRRGAAPERTPVGQGSWAHPGRTRG  
EST2 97 SLFCHSANVNVTLKGAAMKMFHSLVGTYAFVDLLINYTVIQFNGQ-FFTQIVGNRCNEPLPPKQVQRSSSS-----

Euplotes 206 PRCCSTCKYNVKNEDHFLNNI-----NVPNWNMKSRTIFCYTHFNRRNQFF  
HT1 237 PSDRGFCVVSAPPAFEATSLEGALSGTRHSHPSVGRQHAGPPSTSRPPRPWDTPCPVYAETKHFLYSSGDK--EQLR  
EST2 169 ----SATAAQIKQLTEPVTN-----KQFLHKLNIW-SSSFF

Euplotes 255 KKHEFVSNKNNISAM-DRAQTIFTNI-----FRFNIRKKLKDVKIEKIAYMLEKVDFNFNYLTKSCPLPENWRE  
HT1 315 PSFLLSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRY-WQMRPLFELLGNHAQCPYGVLLKTHCPRAAVTP  
EST2 200 PYSKILPSSSIKKLTDLREAIFP-----TNLVKIPQRLKVRINLTQKLLKRHKRLNYVSIINSICPPLEGT--

Telomerase domain

Euplotes 326 RK-----QKIENLINKTREES--KYEEELFSYTTDNKCVTQFINEFFYNILPKDFLTGR-NRKNFQKKVKYVELNKH  
HT1 394 AAGVCAREKPGSVAAPEEEDTDPRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGSRHNERFLRNTKKFISLGKHA  
EST2 268 -----VLDLSHLSRQ-----SPKERVLFIIIVILQKLLPQEMFGSKKNKGKIKNLNLLLSPLNG

Euplotes 398 LIHKNLLEKINTREISWMQVET-SAKHFYFDHENIYVLWKLRLWIFEDLVVSLIRCCFFVTEQQKSYSKTYYYRKNIW  
HT1 474 KLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFVYTETTFQKNRLFFYRKSVM  
EST2 324 YLPFDSLLKKRLKDFRWLFISD-IWFTKHNFENLN-QLAICFISWLFRLIPKIIQTFYCTEIS-STVTIVYFRHDTW

Motif 1 Motif2

Euplotes 477 DVIMKMSIADLKK-ETLAEVQEKEVEEWKSL-GFAPGKLRLIPKKT--FRPIMTFNKKIVNSDRK--TTKLTNTNKL  
HT1 554 SKLQSIGIRQHLKRVQLRELSEAEVRQHREARPAALLTSRLRFIPKPDG--LRPIVNM DYVVGARTFRREKRAERLTSRVK  
EST2 401 NKLITPFI VEYFK-TYLVENNVCRNHSYTLS-NFNHSMRIIPKKSNEFRIIAIPCRGADEEEFT--IYKENHKNAIQ

Fig. 2A



Motif A

Euplates 551 NSHLMKTLKN-RMFKDPFGFAVFNYYDDVMKKYEEFVCKWKVQGQP-KLFFATMDIEKCYDSVNREKLSTFLKTTKLLSS  
HT1 632 ALFSLNYERARR--PGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPN  
EST2 477 PTQKILEYLRNKRPTSFTKIYSPTQIADRIKEFKQRLKKFNNVLP-ELYFMKFDVKSCYDSIPRMECMRILKDALKNEN

Euplates 629 DFWIMTAQILKRKNIVIDSKNFRKKEMKDYFRQKFQKIALEGGQYPTLFSVLENEQNDLNAKKT LIVEAK-GRNYFKND  
HT1 710 TYCVRRYAVVQKAAHGHVRKAFKSHVS-----TLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLNEASSG  
EST2 556 GFFVRSQYFFN-TNTGVLKLFNVVN-----A--SRVPKPYELYIDNVRTVHLSNQDVINVV-EMEIKT-

Motif B

Euplates 708 NLLQPVINICQNYINFNGKFYKQTKGIPQGLCVSSILSSFYATLEESSLGFLRDESMNPENPNVNLMLRLTDDYLLIT  
HT1 777 LFDVFLRFMCHHAVRIR-GKSYVQCQGIQGSILSTLLCSLCYGMEN---KLFAGIRRD-----GLLLRLVDDFLLVT  
EST2 616 --ALWVEDKCYIR-----EDGLFQSSLSAPIVDLVYDDLLEFYSEFKASPSQD-----TLILKLADDFLIIS

Motif C

Motif D

Euplates 788 TQENNAVLFIKLINVSRENGFKFMKKLQTSFPLSPSKFAKYGMDSVEEQNI VQDYCDWIGISIDMKTLALMPNIWLRI  
HT1 847 PHLTHAKTFLRTLVRGVPEYGCVVNLKRTVVNFVDEALGG-TAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYAR--  
EST2 677 TDQQ-QVINIKKLAMG----GFQKYNKANRDKILAVS-----SQSDDDTVIQFCAMHIFVKELEVWKHSSTMV---

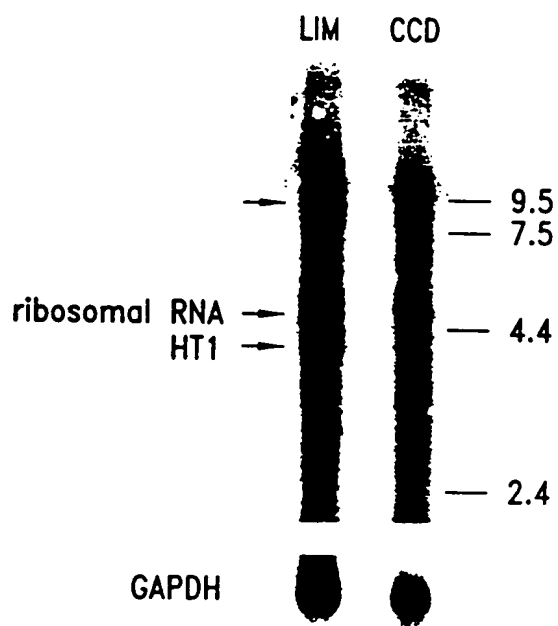
Motif E

Euplates 868 EGILCTLNLMMQTKKASMWLKKKLKSLMNNITHYFRKTITTEDFANKTLNKLFISSGGYKYMQCAKEY--KDHFKKNLAM  
HT1 924 TSIRASLTFRNGFKAGRNMRRLFGVLRKCHSLFLDLQVNSLQTVCTNIYKILLLOAYRFHACVLQLPFHQQVWKNPTF  
EST2 741 -----NFHIRSKSS----KGIFRSLIALFNTRISYKTIDTNLNSTNTVLMQIDHVVKNISECYKSA--FKDLSINVTO

Euplates 946 SSMIDLEVSKIISVTRAFFKYLVCNIKDTIFGEEHYDPFFLSTLKHFIETSTKKYIFNRVCMILKAKEAKLKSDQCQS  
HT1 1004 FLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLC-HQAFLLKLTRHRVTYVPLLSLRTAQTQLSRKLPGT  
EST2 808 NMQFHSFLQRIIEMTVSG----CPITKCDPLIEYEV--FTI--LNGFLESLSNTSKF-KDNIILLRKEIQHLQAYIYI

Euplates 1026 LIQYDA-----  
HT1 1083 TLTALEAAANPALPSDFKTILD  
EST2 879 YIHIVN-----

*Fig. 2B*

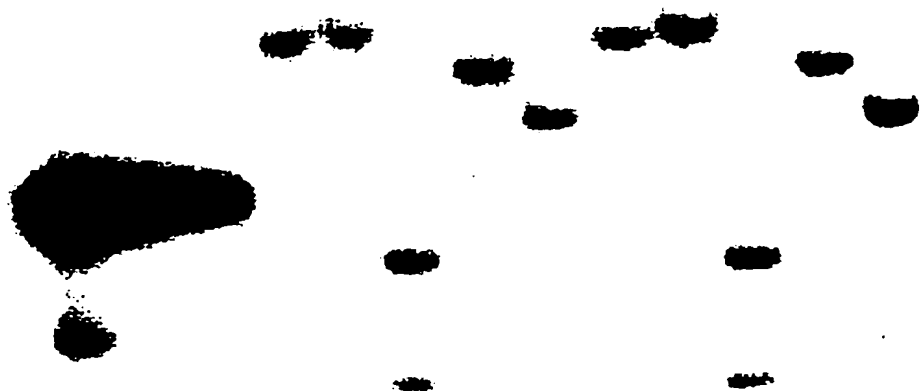


*Fig. 3*

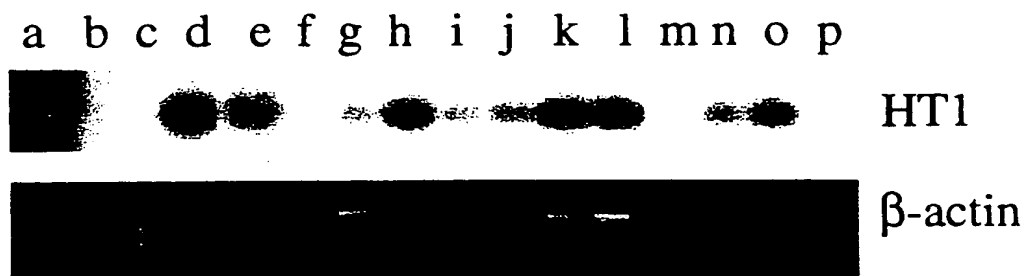




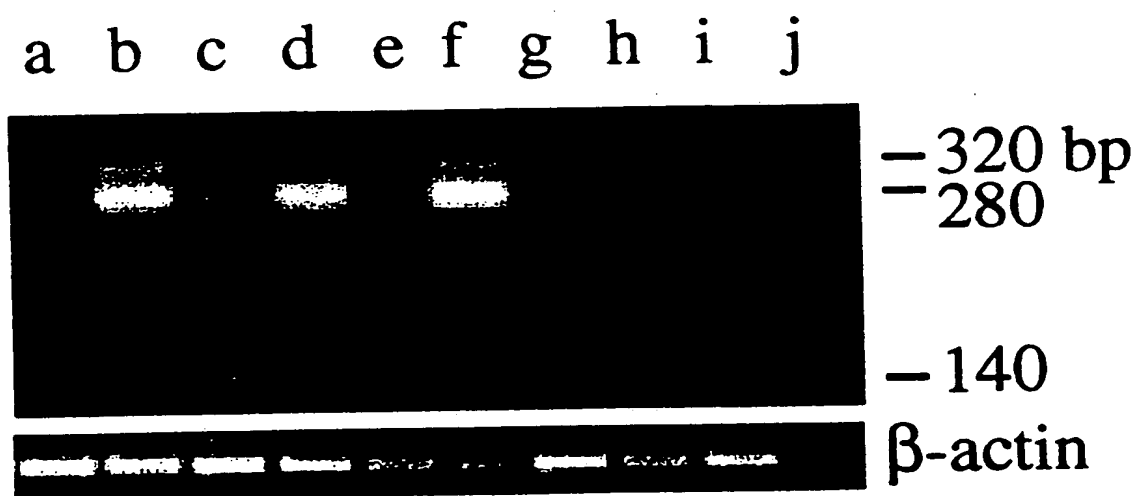
| Plasmid |   |   | Human blood |   |   |   |   | LIM1215 |   |   |   |   |
|---------|---|---|-------------|---|---|---|---|---------|---|---|---|---|
| 10      | 5 | 1 | H           | E | P | X | B | H       | E | P | X | B |



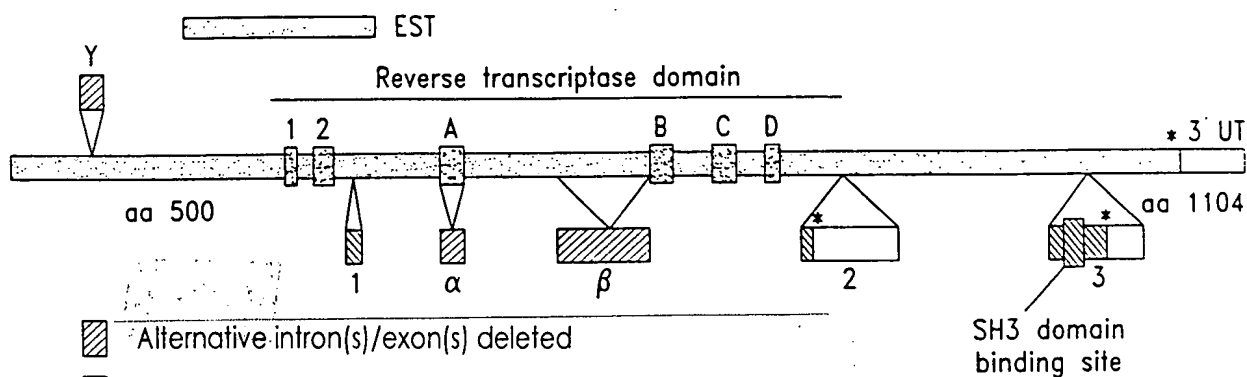
*Fig. 4*



*Fig. 5*



*Fig. 6*



*Fig. 7A*

Variants:

|                       | 1  | $\alpha$ | $\beta$ | 2  | 3     |
|-----------------------|----|----------|---------|----|-------|
| RT-PCR product        | NO | +        | +       | NO | + & - |
| PCR from LIM1215 lib. | -  | +        | -       | +  | NO    |
| RT-PCR product        | NO | -        | +       | NO | +     |
| 53.2 cDNA             | -  | -        | -       | -  | NO    |

*Fig. 7B*



Y 222 5'-CCAGGTG|ggcctc 223 gcaggtg|TCCTGCC-3'

1 1950 5'-AAAGAGG|GTGGCTG.....AACAGAA|GCCGAGC-3' 1952

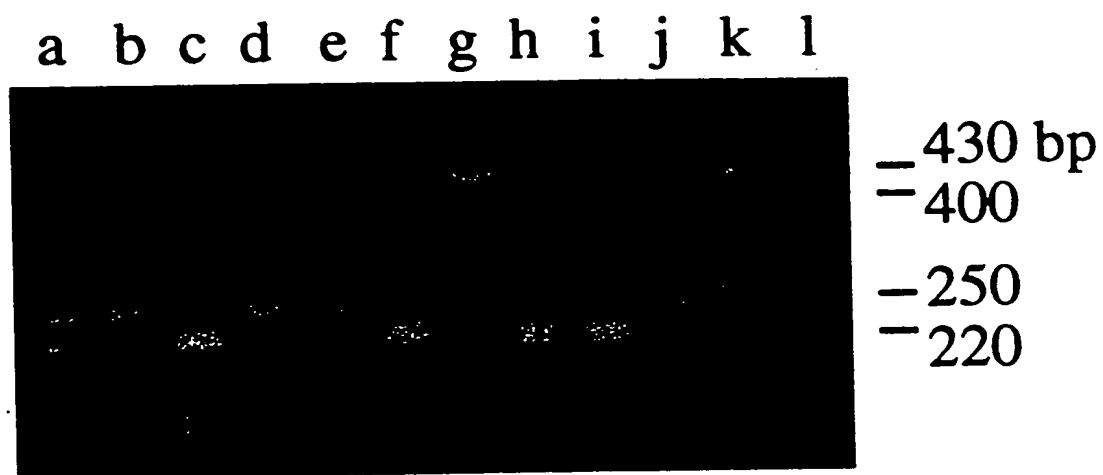
d 2130 5'-TGTC AAG|gtggatg.....ccccag|GACAGGC-3' 2167

b 2286 5'-GAGCCAC|gtctcta.....ggggcaa|GTCCTAC-3' 2468

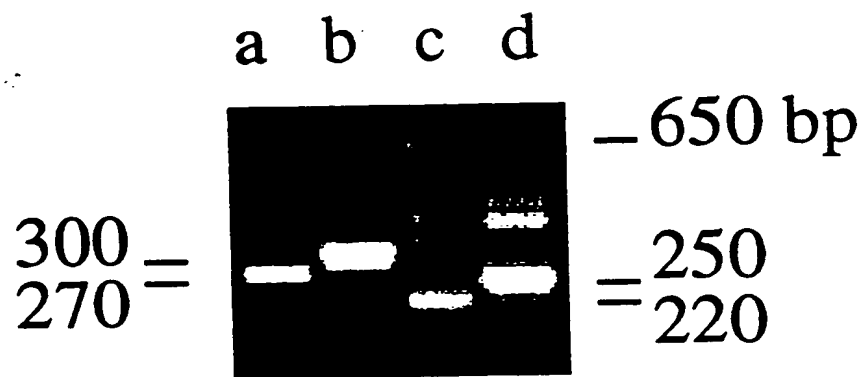
2 2843 5'-ACTCCAG|GTGAGCG.....XXXXXXX|CTATGCC-3' 2844

3 3157 5'-AACGCAG|CCGAAGAAAACATTTCTGTCGTGACTCCTGCGGTGCTTGGGTGCGGACAGCCAGAGATGG  
T A A E E N I L V V T P A V L G S G Q P E M E  
AGCCACCCCGCAGACCGTCGGGTGTGGGCAGCTTTCCGGTGTCTCCTGGGAGGGGAGTTG  
P P R R P S G V G S F P V S P G R G V G  
3158  
GGCTGGGCCTGTGACTCCTCAGCCTCTGTTTTCCCCCAG|GGATGTC-3'  
L G L \*

*Fig. 7C*



*Fig. 8*



*Fig. 9*



sequence "Y" 104-105 bases

GGCCTCCCCGGGGTCGGCGTCCGGCTGGGGTTGAGGGCGGCCGGGGGAACCAG  
GlyLeuProGlyValGlyValArgLeuGlyLeuArgAlaAlaGlyGlyAsnGln  
AlaSerProGlySerAlaSerGlyTrpGly \* GlyArgProGlyGlyThrSer  
ProProArgGlyArgArgProAlaGlyValGluGlyGlyArgGlyGluProAla

CGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCCGCAGGTG  
ArgHisAlaGluSerSerAlaGlyAspSerGlyArgPheProArgArg  
AspMetArgArgAlaAlaGlnAlaThrGlnGlyAlaSerProAlaGly  
ThrCysGlyGluGlnArgArgArgLeuArgAlaLeuProProGlnVal

sequence "1" 38 bases

GTGGCTGTGCTTTGGTTTAACTTCCTTTTTTAACCAGAA  
ValAlaValLeuTrpPheAsnPheLeuPheAsnGlnLys

sequence "α" 36 bases

GTGGATGTGACGGGCGCGTACGACACCATCCCCAG  
ValAspValThrGlyAlaTyrAspThrIleProGln

sequence "β" 182 bases

GTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTG  
ValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu

CAGGAGACCAGCCCGCTGAGGGATGCCGTGTCATCGAGCAGAGCTCCTCCCTG  
GlnGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeu

AATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCAC  
AsnGluAlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHis

GCCGTGCGCATCAGGGGCAA  
AlaValArgIleArgGlyLys

partial sequence "2" unknown length

GTGAGCGCACCTGGCCGGAAGTGGAGCCTGTGCCCGGCTGGGGCAGGTGCTGCTGCAG  
Ter

GGCCGTTGCGTCCACCTCTGCTTCCGTGTGGGGCAGGCGACTGCCAATCCCAAAGGGT  
CAGATGCCACAGGGTGCCCTCGTCCCATCTGGGGCTGAGCACAATGCATCTTTCTG  
TGGGAGTGAGGGTGCCTCACAACGGGAGCAGTTTTCTGTGCTATTTTGGTAA...

*Fig. 10A*





sequence "3" 159 bases

CCGAAGAAAACATTTCTGTCGTGACTCCTGCGGTGCTTGGGTCGGGACAGCCAGAG  
AlaGluGluAsnIleSerValValThrProAlaValLeuGlySerGlyGlnProGlu

ATGGAGCCACCCCGCAGACCGTCGGGTGTGGGCAGCTTTCCGGTGTCTCCTGGGAGG  
MetGluProProArgArgProSerGlyValGlySerPheProValSerProGlyArg

GGAGTTGGGCTGGGCCTGTGACTCCTCAGCCTCTGTTTTCCCCCAG  
GlyValGlyLeuGlyLeu \*

sequence "X" unknown length

...GACAGTCACCAGGGGGTTGACCGCCGACTGGGCGTCCCCAGGGTTGACTATAGGA  
CCAGGTGTCCAGGTGCCCTGCAAGTAGAGGGGCTCTCAGAGGCGTCTGGCTGGCATGG  
GTGGACGTGGCCCCGGGCATGGCCTTCTGCGTGTGCTGCCGTGGGTGCCCTGAGCCCT  
CACTGAGTCGGTGGGGGCTTGTGGCTTCCCGTGAGCTTCCCCCTAGTCTGTTGTCTGG  
CTGAGCAAGCCTCCTGAGGGGCTCTCTATTG

partial sequence of genomic intron (approximately 2.7 kb)

GTGGCTGTGCTTTGGTTTAACTTCCTTTTAAACCAGAAGTGCGTTTGAGCCCCACATT  
TGGTATCAGCTTAGATGAAGGGCCCGGAGGAGGGGCCACGGGACACAGCCAGGGCCAT  
GGCACGGCGCCACCCATTTGTGCGCACAGTGAGGTGGCCGAGGTGCCGGTGCCTCCA  
GAAAAGCAGCGTGGGGGTGTAGGGGAGCTCCTGGGGCAGGGAC....

*Fig. 10B*



## Truncated telomerase

ATGCCGCGCGCTCCCGCTGCCGAGCGGTGCGCTCCCTGCTGCCGAGCCACTACCGCAGGTGCTGCCGCTGGCCACGTTCTGT  
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGCGCGCTGGGGCCAGGGCTGGCGGCTGGTGACGCGGGGACCGGGCTTTCCGCGCGTGGTGCCCACTGCTGGTGCGCTGGGACGACGGCGCCCCCGCGC  
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

CCCCCTCTTCGCGAGGTGCTGCTGAAGGAGCTGGTGCCGAGTGCTGCAGAGGTGCTGCGAGCGCGCGAAGAACGCTGCTGGCTTCGGCTTCGCGCTGCTGGACGGGGCCG  
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCGAGGCTTACCACAGCGTGGCGAGCTACCTGCCAACAGGTGACCGAGCACTGCGGGGAGCGGGGCGTGGGGGCTGCTGCTGCCCGCGTGGGCGACGACGT  
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTTACCTGCTGGCAGCTGCGCGCTTTTGCTGGTGCTGCCAGCTGCGCTACAGGTGCTGCGGGCGCGCTGTACAGCTCGGCGCTGCCACTCAGGCCCGCCCCCGC  
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGACCCCGAAGGCTCTGGGATGCGAACGGGCTGGAACCATAGCGTCAGGAGGCGGGGTCCCTGGGCTGCCAGCCCCGGGTGCGAGGAGCGCGGGGCGAGTGC  
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGTCTGCCGTGCCAAGAGGCCAGGCGTGGCGCTGCCCTGAGCGGAGCGGACGCCCTGGGCGAGGGTCTGGGCGCACCGGGCAGGACGCTGGACCGAGTGACCG  
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTCTGTGTGGTGTCACCTGCCAGACCGCGCGAAGAGCCACCTCTTTGGAGGGTGGCGCTCTCTGGCAGCGCCACTCCACCCATCCGTGGGCGCGCAGCACCGCGGGCCCC  
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGCGGCCACAGCTCCCTGGGACAGCGCTTGTCCCCGGTGTACCGCGAGACCAAGCACTTCTCTACTCTCAGGCGACAAGGAGCAGCTGCGGCCCTCTCTCTACTAG  
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTGAGGCGCAGCTGACTGGCGCTCGGAGGCTCGTGGAGACATCTTTCTGGGTTCCAGGCGCTGGATGCCAGGACTCCCGCAGGTGCCCCGCTGCCAGCGCTACTGGCA  
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATCGGCGCCCTGTTCTGGAGCTGCTGGGAACACGCGAGTGCCCTACGGGGTGTCTCTAAGACGCACTGCCGCTGCGAGCTGCGGTACCCAGCAGCGGTGTCTGTGCCG  
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAAGCCCCAGGGCTGTGTGGCGCCCCGAGGAGGAGACAGACCCCGTGGCTGGTGAGCTGCTCGCCAGCAGCAGCCCCCTGGCAGGTGTACGGTCTGTGCGGGCGTG  
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCGCGGCTGGTGCCCCAGGCTCTGGGGCTCAGGCACAACGACCGCTTCTCAGGAACACCAAGATTATCTCCCTGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCT  
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

GACGTGGAAGATGAGCGTGGGACTGCGCTTGGCTGCGCAGGAGCCAGGGGTTGGCTGTGTTCCGGCGCAGAGCACCCTGCGTGAGGAGATCTGGCCAAGTTCTGCACTGGCT  
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTGTACGTGCTGAGCTGCTCAGGTCTTTCTTTATGTACGGAGACACGTTTCAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAGCATTGG  
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

AAT--NNN--GACAGTCACAGGGGGGTTGACCGCGGACTGGGCGTCCCAGGGTTGACTATAGGACCAGGTGTCCAGGTGCCCTGCAAGTAGAGGGGCTCTCAGAGCGCTGTGGCTGG

*Fig. 11A*



CATGGGTGGACGTGCCCCGGGCATGGCCTTCTGCGTGTGCTGCCGTGGGTGCCCTGAGCCCTCACTGAGTCGGTGGGGCTTGTGGCTTCCCGTGAGCTTCCCCCTAGTCTGTTGTCTG

GCTGAGCAAGCCTCTGAGGGGCTCTATTG...

*Fig. 11B*

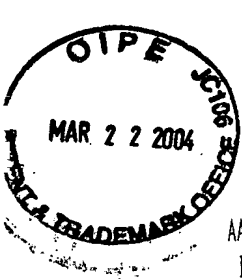


# Truncated protein 1

ATGCCGCGCTCCCGCTGCCGAGCGCTGCGCTCCCTGCTGCGCAGCCACTACCGGAGGTGCTGCCGTGGCCAGTTCTGTG  
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGGCGCTGGGGCCCGAGGCTGGCGGCTGGTGAGCGCGGGACCCGGCGGCTTTCCGCGCTGGTGGCCAGTGCCGTGGTGCGTGCCCTGGGACGACAGGCCGCCCCCGCGG  
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A  
CCCTCCTTCGCCAGGTGCTGCTGAAGGAGCTGGTGGCCGAGTGCTGAGAGGCTGTGCGAGCGCGCGGCGAAGAAGCTGCTGGCTTCGGCTTCGCGCTGCTGGACGGGGCCG  
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R  
CGGGGGCCCCCGAGGCTTCACCACGAGCTGCGCAGCTACCTGCCAACAGGTGACGACGACTGCGGGGAGCGGGGCTGGGGCTGCTGCTGCGCCGCTGGCGACGAGCT  
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V  
GCTGTTACCTGCTGGCAGCTGCGCGCTCTTTGCTGGTGGCTCCAGCTGCGCTTACCAGGTGTGGGGCGCGCTGTACCAGCTCGGCGCTGCCACTCAGGCCGCGCCCCGCG  
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P  
ACAGCTAGTGGACCCGAAGGCTCTGGGATGCGAACGGGCTGGAACCATAGCGTCAGGGAGCGGGGTCCCTGGGCTGCCAGCCCCGGGTGCGAGGAGCGCGGGGCGAGTGC  
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A  
CAGCCGAAGTCTGCCGTTGCCAAGAGGCCGAGCTGCGCTGCGCTGAGCGGAGCGGACGCCGTTGGGCGAGGGTCTGGGCCACCCGGGAGGACGCGTGGACGAGTACCG  
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R  
TGGTTTCTGTGGTGTACCTGCCAGACCCCGGAAGAAGCCACCTCTTTGGAGGGTGGCTCTCTGGCAGCGCCACTCCACCCATCGTGGGCGCCAGCACCGCGGGCCCCC  
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P  
ATCCACATCGCGGCCACCACTCCCTGGGACAGCTTGTCCCCGGTGTACGCGGAGACCAAGCACTTCTCTACTCTCAGGCGACAAGGAGAGCTGCGGGCTCTCTCTACTCAG  
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S  
CTCTCTGAGGCCAGCTGACTGGCGCTCGGAGGCTCGTGGAGACCATTTCTGGGTCCAGGCCCTGGATGCCAGGAGTCCCGCAGGTTGCCCGCTGCCCCAGCGTACTGGCA  
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q  
AATGCGGCCCTGTTTCTGGAGCTGCTTGGGAACACGCGCAGTGCCTTACGGGTGCTCCTCAAGACGCACTGCCGCTGCGAGCTGCGGTACCCAGCAGCGGTGCTGTGCCCC  
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R  
GGAGAAGCCCCAGGCTCTGTGGCGGGCCCCGAGGAGGAGACAGACCCCGTGCCTGGTGAGCTGCTCGCCAGCAGCAGCCCTGGCAGGTGTACGGCTTCTGCGGGCTG  
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C  
CCTGCGCGGCTGGTGGCCCGGCTCTGGGCTCCAGGCACAACGAACGCCGCTTCTCAGGAACCAAGAAGTTCATCTCCTGGGAAGCATGCCAAGCTCTCGCTGAGGAGCT  
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L  
GACGTGAAGATGAGCGTGGGACTGCGCTTGGTGGCAGGAGCCAGGGGTTGGTGTGTTCCGGCGCAGAGCAGCGTCTGCGTGAGGAGATCTGGCCAAGTTCCTGCACTGGCT  
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L  
GATGAGTGTGTACGCTGCTGAGCTGCTCAGGTCTTTCTTTATGTACGGAGACACGTTTCAAAGAAGAGGCTCTTTTCTACCGAAGAGTGTCTGGAGCAAGTGTCAAAGATTGG  
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

Fig. 11C



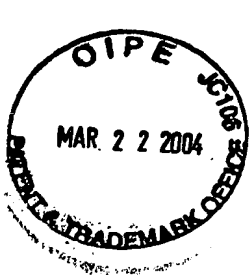
AATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCCGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGA  
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D

GTGGCTGTGCTTTGGTTTAACTTCCTTTTAAACCAGAA

V A V L W F T F L F N Q K

CGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACCTGTTACGCGTGCTCAACTACGA  
G L R P I V N M D Y V V G A R T F R R E K R P S V S F R G \*

*Fig. 11D*



## Truncated protein 2

ATGCCGCGGCTCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCCGAGCCACTACCGGAGGTGCTGCCGTGGCCACGTTTCGTG  
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGGGCGCTGGGGCCCCAGGGCTGGCGGCTGGTGACGCGGGGACCGGGGCTTCCGCGCGCTGGTGGCCAGTGCCGTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCGCCG  
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

CCCCCTCTCCGCCAGGTGCTGCTGAAGGAGCTGGTGGCCGAGTGCTGCAGAGGCTGTGGAGCGCGGCGGAAGAACGTGCTGGCTTCGGCTTCGGCTGCTGGACGGGGCCG  
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCGAGGCTTACCACAGCGTGCGCAGCTACCTGCCCAACACGGTGACGACGACTGCGGGGAGCGGGGCTGGGGGCTGCTGCTGCGCCGCTGGGCGACGACGT  
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTTACCTGCTGGCAGCTGCGCGCTCTTTGCTGGTGGCTCCAGCTGCGGCTACCAAGTGTGCGGGCCGCGCTGTACCAGCTCGGCGCTGCCACTCAGGCCGCGCCCCCGC  
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGGACCCCAAGGCGTCTGGGATGCGAACGGGCTGGAACCATAGCGTCAGGGAGCGCGGGTCCCTTGGGCTGCCAGCCCCGGGTGCGAGGAGGCGGGGGCAGTGC  
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGTCTGCCGTTGCCAAGAGGCCAGGCGTGGCGCTGCCCTGAGCCGAGCGGACGCCGTTGGGAGGGGCTCTGGGCCACCCGGGAGGACGCGTGACCGAGTGACCG  
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTTCTGTGGTGTACCTGCCAGACCCCGCAAGAAGCCACCTCTTTGGAGGGTGCCTCTCTGGCAGCGCCACTCCACCCATCGTGGGCGCCAGCACACGCGGGCCCCC  
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGCGGCCACCACTCCCTGGGACACGCTTGTCCCCGGGTACGCGGAGACCAAGCACTTCTCTACTCTCAGGCGACAAGGAGCAGCTGCGGCCCTCTCTCTACTCAG  
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTCTGAGGCCAGCCTGACTGGCGCTCGGAGGCTCGTGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGACTCCCCGAGGTTGCCCCGCTGCCCGAGCTACTGGCA  
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATGCGGCCCTGTTTCTGGAGCTGCTTGGGAACACGCGCAGTGGCCCTACGGGGTGCTCCTCAAGACGCACTGCCGCTGCGAGCTGCGGTACCCGAGCAGCGGCTGTCTGTGCCG  
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAAGCCCCAGGGCTGTGTGGCGGCCCCGAGGAGGAGACACAGCCCCGTCGCTGGTGACGTGCTCCGCCAGCACAGCAGCCCTGGCAGGTGTACGGCTTCGTGCGGGCTG  
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCGCGGCTGGTGGCCCCAGGCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCTCAGGAACCAAGAAGTTCTCTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCT  
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

GACGTGAAGATGAGCGTGGCGGACTGCGCTTGGCTGCGCAGGAGCCAGGGGTTGGCTGTGTTCCGGCCGAGAGCAGCGTCTGCGTGAGGAGATCTGGCCAAGTTCTGCACTGGCT  
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTGACGTGCTGAGCTGCTCAGGTCTTTCTTTATGTACGGAGACCACTTTCAAAGAAGAGGCTCTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAGCATTGG  
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

Fig. 11E

CCAGGGGATCCCGAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTGGCGGGACGGGCTGCTCCTCGCTTTGGTGA  
P G D P A G L H P L H A A L Q P V L R R H G E Q A V C G D S A G R A A P A F G G  
TGATTTCTGTGGTGACACCTCACCTCACCCACGCGAAAACCTTCCTCAGGACCTGGTCCGAGGTGTCCTCGAGTATGGCTGCGTGGTGAACCTGCGGAAGACAGTGGTGAACCTCC

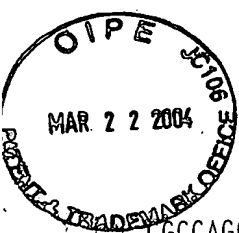


# Reference protein

|  |     |
|--|-----|
| ATGCCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAG   | 60  |
| MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu | 20  |
| GTGCTGCCGCTGGCCACGTTCTGTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCA | 120 |
| ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln | 40  |
| CGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCAGTGCCTGGTGTGCGTGCCCTGG  | 180 |
| ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp | 60  |
| GACGCACGGCCGCCCCCGCCGCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTG    | 240 |
| AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu | 80  |
| GTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGC | 300 |
| ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly | 100 |
| TTGCGCTGCTGGACGGGGCCCGGGGGCCCCCCCCGAGGCCTTACCACCAGCGTGCGC    | 360 |
| PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg | 120 |
| AGCTACCTGCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTG  | 420 |
| SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu | 140 |
| TTGCGCCGCGTGGGCGACGACGTGCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTG | 480 |
| LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal | 160 |
| CTGGTGGCTCCCAGCTGCGCTACCAGGTGTGCGGGCCGCGCTGTACCAGCTCGGCGCT   | 540 |
| LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla | 180 |
| GCCACTCAGGCCCCGGCCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAA | 600 |
| AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu | 200 |
| CGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGT | 660 |
| ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly | 220 |
| GCGAGGAGGCGCGGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCCAAGAGGCCAGGCGT   | 720 |
| AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg | 240 |
| GGCGCTGCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCTGGGCCCACCCGGGC   | 780 |
| GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly | 260 |
| AGGACGCGTGGACCGAGTGACCGTGGTTTCTGTGTGGTGTACCTGCCAGACCCGCCGAA  | 840 |
| ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu | 280 |
| GAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGC | 900 |
| GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly | 300 |

*Fig. 11G*





|  |      |
|--|------|
| CGCCAGCACCACGCGGGCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCCT  | 960  |
| ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro | 320  |
| TGTCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAG  | 1020 |
| CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln | 340  |
| CTGCGGCCCTCCTTCTACTCAGCTCTCTGAGGCCAGCCTGACTGGCGCTCGGAGGCTC   | 1080 |
| LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu | 360  |
| GTGGAGACCATCTTTCTGGGTTCAGGCCCTGGATGCCAGGGACTCCCCGAGGTTGCCC   | 1140 |
| ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro | 380  |
| CGCCTGCCCCAGCGCTACTGGCAAATGCGGCCCTGTTTCTGGAGCTGCTTGGGAACCAC  | 1200 |
| ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis | 400  |
| GCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACC | 1260 |
| AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr | 420  |
| CCAGCAGCCGGTGTCTGTGCCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCCGAGGAG | 1320 |
| ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu | 440  |
| GAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAG | 1380 |
| GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln | 460  |
| GTGTACGGCTTCGTGCGGGCCTGCCTGCGCCGGCTGGTGCCCCAGGCCTCTGGGGCTCC  | 1440 |
| ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer | 480  |
| AGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCAT | 1500 |
| ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis | 500  |
| GCCAAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGGCTGCGCTTGGCTG | 1560 |
| AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu | 520  |
| CGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGAGAGCACCGTCTGCGTGAGGAGATC  | 1620 |
| ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle | 540  |
| CTGGCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTC | 1680 |
| LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe | 560  |
| TTTTATGTCACGGAGACCACGTTTCAAAGAAGCAGGCTCTTTTTCTACCGGAAGAGTGTC | 1740 |
| PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal | 580  |
| TGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTGAAGAGGGTGACGTGCGGGAG   | 1800 |
| TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu | 600  |
| CTGTCGGAAGCAGAGGTCAGGCAGCATCGGAAGCCAGGCCCGCCCTGCTGACGTCCAGA  | 1860 |
| LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg | 620  |

*Fig. 11H*



|   |      |
|---|------|
| CTCCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTG  | 1920 |
| LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal  | 640  |
| GGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCA  | 1980 |
| GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla  | 660  |
| CTGTTCAAGCTGCTCAACTACGAGCGGGCGCGGCCCGCCTCCTGGGCGCCTCTGTG      | 2040 |
| LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal  | 680  |
| CTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAG  | 2100 |
| LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln  | 700  |
| GACCCGCCGCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATC   | 2160 |
| AspProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle  | 720  |
| CCCCAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCAGAACACGTACTGC   | 2220 |
| ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys  | 740  |
| GTGCGTCGGTATGCCGTGGTCCAGAAGGCCGCCATGGGCACGTCCGCAAGGCCTTCAAG   | 2280 |
| ValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys  | 760  |
| AGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTG  | 2340 |
| SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu  | 780  |
| CAGGAGACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAG  | 2400 |
| GlnGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeuAsnGlu  | 800  |
| GCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATC  | 2460 |
| AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle  | 820  |
| AGGGGCAAGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTG  | 2520 |
| ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu  | 840  |
| CTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTGGCGGGAC   | 2580 |
| LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp  | 860  |
| GGGCTGCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCCACGCG  | 2640 |
| GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla  | 880  |
| AAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACCTTG | 2700 |
| LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu  | 900  |
| CGGAAGACAGTGGTGAACCTTCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTT  | 2760 |
| ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal  | 920  |
| CAGATGCCGGCCACGGCCTATTCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTG    | 2820 |
| GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeu  | 940  |

*Fig. 11I*



|  |      |
|--|------|
| GAGGTGCAGAGCGACTACTCCAGCTATGCCCCGACCTCCATCAGAGCCAGTCTCACCTTC | 2880 |
| GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe | 960  |
| AACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGAACTCTTTGGGGTCTTGCGGCTG   | 2940 |
| AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu | 980  |
| AAGTGTCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAAC | 3000 |
| LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn | 1000 |
| ATCTACAAGATCCTCCTGCTGCAGGCGTACAGTTTTACGCATGTGTGCTGCAGCTCCCA  | 3060 |
| IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro | 1020 |
| TTTCATCAGCAAGTTTGAAGAACCCACATTTTTCTGCGCGTCATCTCTGACACGGCC    | 3120 |
| PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAla | 1040 |
| TCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGC | 3180 |
| SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly | 1060 |
| GCCGCCGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCTGCTC  | 3240 |
| AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu | 1080 |
| AAGCTGACTCGACACCGTGTACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAG  | 3300 |
| LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln | 1100 |
| ACGCAGCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGAGCCAAC  | 3360 |
| ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAlaAsn | 1120 |
| CCGGCACTGCCCTCAGACTTCAAGACCATCCTGGAC                         | 3420 |
| ProAlaLeuProSerAspPheLysThrIleLeuAsp                         | 1132 |

*Fig. 11J*



# Truncated protein 3

ATGCCGCGCGCTCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCAGGTGCTGCCGTGCCACGTTCTG  
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGGCGCTGGGGCCAGGGCTGGCGGTGGTGACGCGGGGACCGGGCGGCTTTCGCGCGCTGGTGGCCAGTGCCCTGGTGTGCGTGGCTGGGACGACGGCCGCCCCGCGCG  
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

CCCCTCCTCCGCCAGGTGCTGCTGAAGGAGCTGGTGGCCGAGTGTGACAGGCTGTGCGAGCGGGCGCAAGAACGTGCTGGCTTCGGCTTCGCGCTGTGGACGGGGCCG  
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCGAGGCTTACCACAGCGTGGCAGCTACCTGCCAACACGGTGACCGACGACTGCGGGGAGCGGGGCTGGGGGTGCTGCTGCGCGCTGGGCGACGAGCT  
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGTTACCTGCTGGCAGCTGCGCGCTTTTGTGCTGGTGGCTCCAGCTGCGCTTACCAGGTGTGCGGGCCGCGCTGTACCAGCTCGGCGTGGCACTAGGCCCCGGCCCCGCG  
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACAGCTAGTGAGCCCCGAAGGCTCTGGGATGCGAAGGGCTGGAACCATAGCGTACGGGAGCGGGGCTCCCTGGGCTGCCAGCCCCGGGTGCGAGGAGCGCGGGGCGAGTGC  
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGTGTGCGTTGCCAAGAGGCCAGGCGTGGCGCTGCCCTGAGCGGAGCGGACGCCGTTGGGAGGGGTCTGGGCCACCCGGGCGAGGACGCTGGACGAGTGACCG  
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTTCTGTGGTGTACCTGCCAGACCCGCGAAGAAGCCACCTCTTTGAGGGGTGCGCTCTGCGACGCGCCACTCCACCCATCCGTGGGCGCCAGCACCACGCGGGCCCCC  
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGCGGCCACCGCTCCCTGGGACAGCCTTGTCCCCGGGTACGCCGAGACCAAGCACTTCTCTACTCTCAGGCGACAAGGAGCAGCTGGCGCCCTCTCTACTCAG  
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTCTGAGGCCAGCCTGACTGGCGCTCGGAGGCTCGTGAGACCATTTCTGGGTTCCAGGCCCTGGATGCCAGGACTCCCCGAGGTTGCCCCGCTGCCCCAGCGCTACTGGCA  
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATCGGCCCCGTGTTCTGGAGCTGCTTGGGAACACGCGCAGTCCCCACGGGGTGTCTCAAGACGCACTGCCGCTGCGAGCTGCGGTACCCGAGCAGCGGTGTCTGTGCCCG  
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

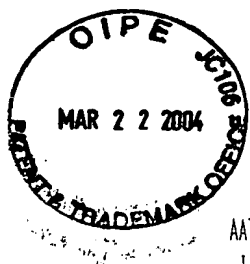
GGAGAAGCCCCAGGGCTCTGTGGCGCCCCGAGGAGGAGACAGACCCCGTCCCTGGTGCAGCTGCTCCGCGACACAGCAGCCCTGGCAGGTGTACGGCTCTGTGCGGGCTG  
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CTGCGCGGCTGGTGGCCCCAGGCTCTGGGGTCCAGGCACAACGAACGCCCTTCTCAGGAACCAAGAAGTTCATCTCCCTGGGAAGCATGCCAAGCTCTGCTGCAGGAGCT  
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

GACGTGAAGATGAGCGTGGGACTGCGCTTGGTGGCAGGAGCCAGGGGTGGCTGTGTTCCGGCGCAGAGCACCCTGCGTGAGGAGATCTGGCAAGTTCCTGCAGTGGCT  
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTGTAGCTGCTGAGCTGCTCAGGCTTTCTTTTATGTACGAGACACGTTTCAAAGAACAGGCTCTTTTCTACCGAAGAGTGTCTGGAGCAAGTGTCAAAGATTGG  
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

Fig. 11K



AATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTGGAAGCAGAGGTGAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCAAGCCTGA  
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D

CGGGCTGCGGCCGATTGTGAACATGGACTACGTGCTGGGAGCCAGAAGCTTCGCGAGAGAAAAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTACGGTGTCTAACTACGA  
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E

GCGGGCGCGGCCCGCCGCTCTGCTGGGCGCTGTGCTGGGCGCTGGACGATCCACAGGGCCTGGCGCACCCTTCGTGCTGCGTGTGCGGGCCAGGACCCGCGCCTGAGCTGTACTT  
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P E L Y F

TGTCAAGGTGGATGTGACGGGCGGTACGACACCATCCCCAGGACAGGCTCAGGAGGTGATCGCCAGCATCATCAAACCCAGAACAGTACTGCGTGCCTGCGTATGCCGTGGTCCA  
V K V D V T G A Y D T I P Q D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q

GAAGGCCGCCATGGGCAGTCCGCAAGGCTTCAAGAGCCAGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTGCTGGCTCACCTGACGAGAGACCAGCCCGCTGAGGGA  
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D

TGCCGTGCTATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGGCAAGTCTACGTCCAGTG  
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C

CCAGGGGATCCCGAGGGCTCCATCCTCTCCACGTGCTGTGACGCTGTGCTACGGCGACATGGAGAACAGCTGTTGCGGGGATTGCGGGGACGGGCTGCTCCTGCGTTTGGTGA  
Q G I P Q G S I L S T L L C S L C Y G D M E N K L F A G I R R D G L L L R L V D

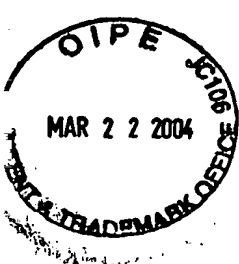
TGATTTCTGTTGGTGACACCTCACCTCACCCACGCGAAAACCTTCTCAGGACCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACCTTGCAGGAGACAGTGGTGAACCTCCC  
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P

TGTAGAAGACGAGGCCCTGGGTGGCAGGCTTTTGTTCAGATGCCGGCCACGGCCTATTCCCTGGTGGGCTGCTGCTGGATACCCGGACCTGGAGGTGCAGAGCGACTACTCCAG  
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S R

GTGAGCGCACCTGGCCGGAAGTGAGCCTGTGCCCCGCTGGGGCAGGTGCTGCTGCAGGGCGTTGCGTCCACCTCTGCTTCCGTGTGGGGCAGGCGACTGCCAATCCCAAGGGTCAGA  
\*

TGCCACAGGGTGCCCTCGTCCATCTGGGGCTGAGCACAAATGCATCTTTCTGTGGAGTGAGGGTGCCTCACAACGGGAGCAGTTTTCTGTGCTATTTTGGTAA....

Fig. 11L



## Altered C-terminus protein

ATGCCGCGCGCTCCCCGCTGCCGAGCGTGCCTCCCTGCTGCCGAGCCACTACCGCAGGTGCTGCCGCTGGCCACGTTCTGT  
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGGCGCTGGGGCCCCAGGGCTGGCGGCTGGTGACGCGCGGGACCCGGCGGCTTCCGCGCGTGGTGGCCCACTGCCCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCGCGC  
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

CCCCCTCTCCGCCAGGTGCTGCTGAAGGAGCTGGTGGCCGAGTGTGCAGAGGCTGTGCGAGCGCGCGCAAGAACGTGCTGGCTTCGGCTTCGCGCTGCTGGACGGGGCCCG  
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCGAGGCTTACCACAGCGTGCAGCTACCTGCCAACACGGTGACGACGACTCGGGGGAGCGGGGCTGGGGGCTGCTGCTGCGCCGCTGGGCGACGACGT  
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTTCACGTGCTGGCAGCTGCGCGCTTTTGTGCTGGTGGCTCCCACTGCGGCTACCAGGTGTGCGGGCCGCGCTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGGCCCCCGC  
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGGACCCCAAGGCGTCTGGGATGCGAACGGGCTGGAACCATAGCGTCAAGGAGCGCGGGTCCCCCTGGGCTGCCAGCCCCGGGTGCGAGGAGGCGGGGGCAGTGC  
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGTCTGCCGTTGCCAAGAGGCCAGGCGTGGCGCTGCCCTGAGCGGAGCGGACGCCGTTGGGAGGGGTCTGGGCCACCCGGGAGGACGCGTGACCGAGTGACCG  
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTTCTGTGGTGTACCTGCCAGACCCGCCAAGAAGCCACCTCTTTGGAGGGTGCCTCTCTGGCAGCGCCACTCCACCCATCGTGGGCCCGCAGCACCACGGGGCCCCC  
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGCGGCCACCACGTCCTGGGACACGCTTGTCCCCGGGTACGCGGAGACCAAGCACTTCTCTACTCTCAGGCGACAAGGAGCAGCTGCGGCGCTCTCTCTACTCAG  
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTCTGAGGCCAGCCTGACTGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTCCAGGCCCTGGATGCCAGGACTCCCCGAGGTTGCCCGGCTGCCCGAGCGTACTGGCA  
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATGCGGCCCCGTGTTCTGGAGCTGCTTGGGAACACGCGCAGTCCCCCTACGGGGTGTCTCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTACCCAGCAGCGGCTGTGTGCCCC  
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

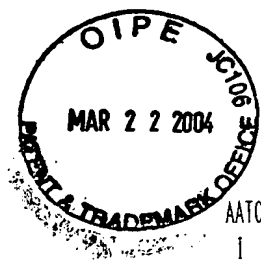
GGAGAAGCCCCAGGGCTCTGTGGCGGCCCCGAGGAGGAGACAGACCCCCGCTCGCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCTGGCAGGTGTACGGCTTCGTGCGGGCTG  
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCGCGGCTGGTGGCCCCAGGCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCTCAGGAACCAAGAAGTTTCATCTCCCTGGGAAGCATGCCAAGCTCTCGTGCAGGAGCT  
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

GACGTGAAGATGAGCGTCCGGGACTGCGCTTGGCTGCGCAGGAGCCAGGGGTGGCTGTGTTCCGGCGCAGAGCAGCGTCTGCGTGAGGAGATCCTGGCCAAGTTCTGCACTGGCT  
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTGACGTGCTGAGCTGCTCAGGCTTTTCTTTATGTACGGAGACCACGTTTCAAAGAAGAGGCTTTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAGATTGG  
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

*Fig. 11M*



AATCAGACGCACTTGAAGAGGTGCAGCTGCGGGAGCTGTGGAAGCAGAGGTGAGGCAGCATCGGAAGCCAGGCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCAAGCCTGA  
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D

CGGGCTGCGGCCGATTGTGAACATGGACTACGTCTGGGAGCCAGAAGCTTCGCGAGAGAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTACGCGTCTCAACTACGA  
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E

GCGGGCGCGGCCGCCGCTCTGCTGGGCGCTGTGCTGGGCTGGACGATATCCAGGGCCTGGCGCACCCTTCTGCTGCGTGTGCGGGCCAGGACCCGCCGCTGAGCTGTACTT  
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P E L Y F

TGTCAGGTGGATGTGACGGGCGGTACGACACCATCCCCAGGACAGGCTCAGGAGGTATCGCCAGCATCATCAAACCCAGAACAGTACTGCGTGGTGGTATGCCGTGGTCCA  
V K V D V T G A Y D T I P Q D R L T E V I A S I I K P O N T Y C V R R Y A V V Q

GAAGGCCGCCATGGGACGTCCGCAAGGCTTCAAGAGCCAGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGTCTCACCTGCAGGAGACCAGCCGCTGAGGGA  
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D

TGCCGTGCTATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGGCAAGTCTACGTCCAGTG  
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C

CCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCCTGTGCTACGGGACATGGAGAACAGCTGTTTGGGGATTGCGGGGACGGGCTGCTCTGCGTTTGGTGA  
Q G I P Q G S I L S T L L C S L C Y G D M E N K L F A G I R R D G L L L R L V D

TGATTTCTGTGGTGACACCTCACCTCACCCACGGGAAACCTTCTCAGGACCTGGTCCGAGGTGCTCCTGAGTATGGCTGCGTGGTGAACCTGCGGAAGACAGTGGTGAACCTCCC  
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P

TGTAGAAGACGAGGCCCTGGGTGGCAGGCTTTTGTTCAGATGCGGGCCACGGCCTATTCCCTGGTGGGCTGCTGCTGGATACCCGGACCTGGAGGTGCAGAGGCACTACTCCAG  
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S S

CTATCCCGGACCTCCATCAGAGCAGTCTCACCTTCAACCGGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGCTTTCGGCTGAAGTGTACAGCCTGTTTCTGGA  
Y A R T S I R A S L T F N R G F K A G R N M R R K L F G V L R L K C H S L F L D

TTTGAGGTGAACAGCCTCAGACGGTGTGCACCAACATCTACAAGATCTCTGCTGCTGAGGCTACAGGTTTACGCATGTGTGCTGCAGTCCCATTTTCATCAGCAAGTTTGAAGAA  
L Q V N S L Q T V C T N I Y K I L L L Q A Y R F H A C V L Q L P F H Q Q V W K N

CCCCACATTTTCTGCGGTGATCTCTGACAGGCTCCCTCTGCTACTCCATCTCTGAAAGCCAGAAGCAGGGATGTGCTGGGGGCCAAGGGCGCCGCCGCTCTGCTCCCTCCGA  
P T F F L R V I S D T A S L C Y S I L K A K N A E

1  
CCGAAGAAAACATTTCTGCTGACTCTGCGGTGCTTGGGTC  
E E N I L V V T P A V L G S

GGGACAGCCAGAGATGGAGCCACCCCGCAGACCGTGGGTGTGGGAGCTTTCCGGTGTCTCTGGGAGGGAGTTGGGCTGGGCTGTGACTCCTCAGCCTCTGTTTTCCCCCAG  
G Q P E M E P P R R P S G V G S F P V S P G R G V G L G L \*

Fig. 11N



# Protein that lacks motif A

ATGCCGCGCGCTCCCCGCTGCCGAGCGTGGCGTCCCTGCTGCCGAGCCACTACCGGAGGTGCTGCCGCTGGCCACGTTGCTG  
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGGCGCTGGGGCCCCAGGGCTGGCGGCTGGTGACGCGGGGACCCGGCGGCTTCCGCGCGTGGTGGCCAGTGCCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCGCGC  
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

CCCCCTCTCCGCCAGGTGCTGCTGAAGGAGCTGGTGGCCGAGTGTGACAGGCTGTGCGAGCGCGCGGAAGAACGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCG  
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCGAGGCTTACCACAGCGTGGCAGCTACCTGCCAACACGGTGACGACGACTCGGGGGAGCGGGCGTGGGGGCTGCTGCTGCGCCGCTGGGCGACGAGCT  
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTTCACCTGCTGGCAGCTGCCGCTCTTTGCTGGTGGCTCCAGCTGCGCTACCAGGTGTGGGGCGCGCTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGGCCCCCGC  
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACAGCTAGTGGACCCGAAGGCGTCTGGGATGCGAACGGGCTGGAACCATAGCTCAGGAGGCGGGGTCCCCCTGGGCTGCCAGCCCCGGGTGCGAGGAGCGCGGGGCGAGTGC  
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCGAAGTCTGCCGTTGCCAAGAGGCCAGGCGTGGCGTGGCCCTGAGCGGAGCGGACGCGGTTGGGCGAGGGTCTGGGCCACCCGGGCGAGACCGTGGACGAGTGACCG  
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTTCTGTGGTGTACCTGCCAGACCCGCGAAGAAGCCACCTCTTTGGAGGGTGGCGTCTCTGGCAGCGCCACTCCACCCATCCGTGGGCGCCAGCACCAGCGGGGCCCCC  
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGCGGCCACCACGCTCCCTGGGACAGCCTTGTCCCCGGGTACGCCGAGACCAAGCACTTCTCTACTCTCAGGCGACAAGGAGCAGTGGGGCCCTCTCTACTCAG  
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTCTGAGGCGCAGCCTGACTGGCGCTCGGAGGCTCGTGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCGCAGGTTGCCCGCCTGCCCGAGCCTACTGGCA  
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATCGGGCCCTGTTTCTGGAGCTGCTTGGGAACACGCGCAGTGGCCCTACGGGTGCTCTCAAGACGCACTGCCGCTGCGAGCTGCGGTACCCAGCAGCCGGTGTGTGCGCCG  
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAAGCCCCAGGGCTCTGTGGCGCCCCGAGGAGGAGACAGACCCCGTGGCTGGTGCAGCTGCTCCGCCAGCAGCAGCCCTGGCAGGTGTACGGCTTCTGTGGGGCTG  
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCGCGGCTGGTGGCCCGAGGCTCTGGGGCTCCAGGCACAACGAACGCGCTTCTCAGGAACACCAAGAAGTTCATCTCCCTGGGAAGCATGCCAAGCTCTCGTGCAGGAGCT  
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

GACGTGAAGATGAGCGTGGGACTGCGCTTGGCTGCGCAGGAGCCAGGGGTGGCTGTGTCCGGCGCAGAGCACCCTGCGTGAGGAGATCTGGCCAAAGTCTCGTGCAGGAGCT  
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTACGCTGCTGAGCTGCTCAGGCTTTTCTTTATGTACGGAGACCAGGTTTCAAAGAACAGGCTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTCAAAGCATTGG  
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

Fig. 110



AATCAGACAGCACTTGAAGAGGGTGCAGCTGCCGGAGCTGTTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCTGA  
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D

CGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTACCTCGAGGGTGAAGGCACTGTTACAGCGTGCTCAACTACGA  
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E

GCGGGCGCGGCCCGCCCGGCTCTCTGGGCGCTCTGTGCTGGGCTGGACGATATCCACAGGGCTGCGGCACCTTCGTGCTGCGTGTGCGGGCCAGGACCCGCCCTGAGCTGACTT  
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F

GTCAAG V K GACAGGCTCACGGAGTGCATGCCAGCATCATCAAACCCAGAACACGTAAGTGCCTGCGTGGTATGCCGTGGTCCA  
D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q

GAAGGCCGCCCATGGGCACGTCGCGAAGGCTTCAAGAGCCACGTCCTCTACCTTGACAGACCTCCAGCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAGACCAGCCCGCTGAGGGA  
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D

TGCGCTGCTCATGAGCAGAGCTCTCTCTGAATGAGGCCAGCAGTGGCTCTTCGACGCTTCTCTACGCTTCATGTGCCACCAGCGGTGCGCATCAGGGGCAAGTCTACGTCAGTG  
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C

CCAGGGGATCCCGCAGGGCTCCATCTCTCCAGCTGCTCTGACGCTGTGCTACGGCGACATGGAGAACAAGTGTGTTGCGGGGATTGCGCGGACGGGCTGCTCTCGCTTTGGTGGGA  
Q G I P Q G S I L S T L L C S L C Y G D M E N K L F A G I R R D G L L L R L V D

TGATTTCTTGTGGTGACACCTCACCTCACCCACGCGAAAACCTTCTCAGGACCTGGTCCGAGGTGTCCTGAGTATGGCTGCGTGGTGAACCTGCGGAAGACAGTGGTGAACCTCCC  
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P

TGTAGAAGACGAGGCCCTGGGTGGCAGGCTTTTGTTCAGATGCCGGCCACGGCTATTCCCTGGTGGCGCTGCTGCTGGATACCCGACCTTGGAGGTGCAGAGCGACTACTCCAG  
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S S

CTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCGGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGGCGCTGAAGTGCACAGCCTGTTTCTGGA  
Y A R T S I R A S L T F N R G F K A G R N M R R K L F G V L R L K C H S L F L D

TTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTACAAGATCTCTGCTGCAAGCGTACAGGTTTACGACATGTGTGCTGCAAGTCTCCATTTTCATCAGCAAGTTTGAAGAA  
L Q V N S L Q T V C T N I Y K I L L L Q A Y R F H A C V L Q L P F H Q Q V W K N

CCCCACATTTTCTGCGCGTCATCTCTGACAGGCTCTCTCTGCTACTCCATCTGAAAGCCAGAAGCAGGAGTGTGCTGGGGGCCAAGGGCGCCGCCGCTCTGCTCTCCGA  
P T F F L R V I S D T A S L C Y S I L K A K N A G M S L G A K G A A G P L P S E

GGCCGTGCAAGTGGTGTGCCACCAAGCATTCTGCTCAAGCTGACTCGACACCGTGCACCTACGTCGCACTCTGGGGTCACTCAGGACAGCCAGACGCACTGAGTCGGAAGCTCCC  
A V Q W L C H Q A F L L K L T R H R V T Y V P L L G S L R T A Q T Q L S R K L P

GGGGACGACGCTGACTGCCCTGGAGGCCGACGCAACCCGGCACTGCCCTCAGACTTCAAGACCATCTGGACTGATGGCCACCCGCCACAGCCAGGCCGAGAGCAGACACCAGCAGCC  
G T T L T A L E A A A N P A L P S D F K T I L D

CTGTACGCGCGGCTCTACGTCAGGGAGGGAGGGGCGGCCACACCCAGGCGCCGACCGCTGGGAGTCTGAGGCTGAGTGAGTGTGTTGGCCGAGGCTGCATGTCCGGCTGAAGGCT  
GAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCAAGGGCTGAGTGTCCAGCACACCTGCCGTCTCACTTCCCACAGGCTGGCGCTGGCTCCACCCAGGGCGAGCTTTTCTCAC

CAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGATTGCCATTGTTCAACCTCGCCCTGCCCTCTTTGCTTCCACCCCAACCATCCAGGTGGAGACCTGAGAA

*Fig. 11P*



GGACCTGGGAGCTCTGGGAATTTGGAGTGACCAAGGTGTGCCCTGTACACAGGCGAGGACCTGCACCTGGATGGGGTCCCTGTGGGTCAAATTGGGGGAGGTGCTGTGGGAGTAA  
AATACTGAATATATGAGTTTTTCAGTTTTGA

*Fig. 11Q*



# Truncated protein that lacks motif A

ATGCCGCGCGCTCCCGCTGCCGAGCGTGGCGTCCCTGCTGCGCAGCCACTACCGGAGGTGCTGCCGCTGGCCACGTTCTGTG  
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGGCGCTGGGGCCCCAGGGCTGGGGCTGGTGACGCGGGGACCCGGCGCTTTCCGCGCGTGGTGGCCAGTGCCTGGTGTGCGTGCCTGGGACGACGGCCGCCCCCGCGC  
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

CCCCCTCTCCGCCAGGTGCTGCTGAAGGAGCTGGTGGCCGAGTGTGCGAGGCTGTGCGAGCGCGGCGGAAGAAGTGTGCTGCGCTTCGGCTTCGCGTGTGACGGGGCCCG  
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCGAGGGCTTACCACGAGCGTGGCAGCTACCTGCCAACACGGTGACGACGCACTGCGGGGAGCGGGCGTGGGGCTGCTGCTGCGCGCGTGGGACGACGCT  
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTTACCTGCTGGCAGCTGCGCGCTCTTTGTGCTGGTGGCTCCAGCTGCGCTACAGGTGTGCGGGCGCGCTGTACCAGCTGCGCGTGCCTACGAGCCGGCCCCCGCC  
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGGACCCCGAAGCGTCTGGGATGCGAACGGGCTGGAACCATAGCGTCAGGAGGCGGGGTCCCTGGGCTGCGAGCCCGGGTGGAGGAGCGGGGGCAGTGC  
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCGAAGTCTGCCGTTGCCAAGAGGCCAGGCGTGGCGCTGCCCTGAGCGGAGCGGACCGCGTGGGCGAGGGTCTGGGCGCCACCGGGCAGGACGCGTGGACGAGTGACCG  
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTTCTGTGGTGTACCTGCCAGACCCCGGAAGAAGCCACCTCTTTGGAGGGTGGCTCTCTGGCACGCGCACTCCACCCATCCGTGGGCGCCAGCACCACGCGGGCCCCC  
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGCGCCACCAGTCCCTGGGACACGCTTGTCCCCGGTGACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGTGGCGCCCTCTTCTACTCAG  
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTCTGAGGCCAGCCTGACTGGCGCTCGGAGGCTCGTGGAGACCATCTTTTGGGTTCCAGGCCCTGGATGCCAGGACTCCCGCAGGTTGCCCCGCTGCCAGCGCTACTGGCA  
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATCGGCGCCCTGTTTCTGGAGTGTCTGGGAACACGCGCAGTGGCCCTACGGGCTGCTCCTCAAGACGCACTGCCGCTGCGAGCTGCGGTACCCAGCAGCGGTGTGTGTGCCG  
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

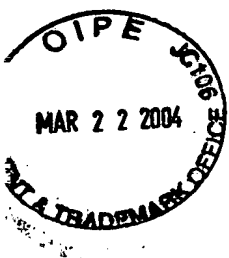
GGAGAAGCCCCAGGGCTCTGTGGCGGGCCCCGAGGAGGAGACAGACCCCGTGGCTGGTGCAGTGTCTCCGACGACAGCAGCCCTGGCAGGTGTACGGCTTCTGTGGCGGCTG  
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCGCGGCTGGTCCCCAGGCTCTGGGGCTCCAGGCACAACGACCGCTTCTCAGGAACACCAAGAAGTTCTCTCCCTGGGAAGCATGCCAAGTCTCTGTCGAGGAGCT  
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

GACGTGAAGATGAGCGTGGGACTGCGCTTGGCTGCGCAGGAGCCAGGGGTTGGCTGTGTTCCGCGCGCAGAGCACCCTGCGTGAGGAGATCTGGCCAAGTCTCTGCACTGGCT  
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTGTACGTCGTGAGCTGCTCAGGTCTTTCTTTTATGTACGGAGACCAGTTTCAAAGAAGAGGCTCTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG  
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

Fig. 11R



AATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTGGAAGCAGAGGTGAGGCAGCATCGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCAAGCCTGA  
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D

CGGGCTGCGGCCGATTGTGAACATGGACTACGTGCGGGAGCCAGAAGCTTCGCGAGAGAAAAGAGGCCGAGCGTCTCACCTCGAGGGTGAAGGCAGTGTTCAGCGTGTCAACTACGA  
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E

GCGGGCGCGGCCCGCCCTCTGGGCGCTGTGCTGGGCTGGACGATATCCAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCAGGAGCCGCGCTGAGCTGTACTT  
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F

TGTCAAG  
V K

GACAGGCTCAGGAGGTGATCGCCAGCATCATCAACCCAGAACAGTACTGCGTGGTGGTATGCCGTGGTCCA  
D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q

GAAGGCCGCCCATGGGCAGCTCCGCAAGGCCTTCAAGAGCCAGTCTCTACCTTGACAGACCTCCAGCCGTACATGCCAGAGTTCGTGGCTCACCTGCAGGAGACGAGCCGCTGAGGGA  
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D

TGCCGTGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTGGCCTCTTCGACGCTTCTACGCTTCATGTGCCACCAGCCGTGCGCATCAGGGGCAAGTCTACGTCCAGTG  
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C

CCAGGGGATCCCGAGGGCTCCATCCTCTCCAGCTGCTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGGGGGATTGCGGGGACGGGCTGCTCCTGCGTTTGGTGGA  
Q G I P Q G S I L S T L L C S L C Y G D M E N K L F A G I R R D G L L L R L V D

TGATTTCTTGTGGTGACACCTCACCTCACCCAGCGAAAACCTTCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAAGTTCGGAAGACAGTGGTGAAGTTCCTC  
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P

TGTAGAAGACGAGGCCCTGGGTGGCAGGCTTTTGTTCAGATGCCGGCCACGGCCTATTCCTGCTGGTGGCCTGCTGCTGGATACCGGACCCTGGAGGTGCAGAGCGACTACTCCAG  
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S R

GTGAGCGCACCTGGCCGGAAGTGGAGCCTGTGCCGGCTGGGGCAGGTGCTGCTGCAGGGCCGTGCGTCCACCTCTGCTTCGCTGTGGGGCAGGCGACTGCCAATCCCAAGGGTCAGA  
\*

TGCCACAGGGTGCCCTCGTCCCATCTGGGGCTGAGCACAAATGCATCTTTCTGTGGGAGTGAGGGTGCCCTCACAACGGGAGCAGTTTTCTGTGCTATTTTGGTAA...

*Fig. 11S*



# Lacks motif A and altered C-terminus

ATGCCGCGCGCTCCCGCTGCCGAGCGGTCCGCTCCCTGCTGCGCAGCCACTACCGGAGGTGCTGCCGCTGCCACGTTCTGTG  
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGGCGCTGGGGCCAGGGCTGGCGGCTGGTGCAGCGGGGACCGGGCGCTTTCCGCGCTGGTGGCCAGTGCCTGGTGTGCGTGCCTGGGACGCACGGCGCCCGCCCGCGC  
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

CCCCCTCTCCGCCAGGTGTCTGCTGAAGGAGCTGGTGGCCGAGTGTGCAGAGGCTGTGCGAGCGCGGCGGAAGAACGTGCTGGCCTTCGGCTTCGCGCTGTGGACGGGGCCCG  
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCGAGGCTTACCACACGCTGCCGAGCTACCTGCCAACACGGTGACCGACGCACTCGGGGGAGCGGGCGTGGGGGCTGCTGCGCGCGCTGGGCGACGACGT  
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGTTTCACTGCTGGCAGCTGCCGCTCTTTGTGCTGGTGGCTCCAGCTGCCCTACCAGGTGTGCGGGCGCGCTGTACCAGCTCGGCGTGCCTCAGGCCCGGGCCCCCGC  
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGGACCCCGAAGCGCTCTGGGATGCGAACGGGCTGGAACCATAGCGTCAGGGAGGCGGGGTCCCTGGGCTGCGACGCCCGGGTGCAGGAGGCGGGGGCAGTGC  
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCGAAGTCTGCCGTTGCCAAGAGGCCAGGCGTGGCGCTGCCCTGAGCGGAGCGGACGCCGTTGGGCGAGGGTCTGGGCCACCCGGGCGAGGCGGTGGACCGAGTGACCG  
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTTCTGTGTGTACCTGCCAGACCCGCCAAGAAGCCACCTCTTTGAGGGTGCGCTCTCTGCGACGCGCACTCCACCCATCCGTGGGCGCCAGCACCACGGGGCCCCC  
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGGGCCACCAGTCCCTGGGACACGCTTGTCCCCGGTGACGCCGAGACCAAGCACTTCTCTACTCTCAGGCGACAAGGAGAGCTGGGCGCTCTCTCTACTCAG  
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTGAGGCGCAGCTGACTGGCGCTCGGAGGCTCGTGAGACCATCTTTCTGGGTTCAGGCGCTGGATGCCAGGGACTCCCGCAGGTTGCCCGCTGCCCGAGCGTACTGGCA  
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATGCGCCCTGTTTCTGGAGCTGCTTGGGAACACGCGCAGTGCCCTACGGGTGCTCTCAAGACGCACTGCCGCTGCGAGCTGCGGTACCCAGCAGCGGTGTCTGTGCCG  
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAAGCCCCAGGCTCTGTGGCGGCCCCGAGGAGGAGACAGACCCCGTCCCTGGTGCAGCTGCTCCGCCAGCAGCAGCCCCCTGGCAGGTGTACGGCTTCTGTGGGCGCTG  
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCGCGGCTGGTCCCCAGGCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCTCAGGAACACCAAGAAGTTATCTCCCTGGGGAAGCATGCCAAGCTCTCGTGCAGGAGCT  
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

GACGTGAAGATGAGCGTGGGACTGCGCTTGGCTGCGCAGGAGCCAGGGGTGGCTGTGTTCCGGCGCAGAGCAGCGTCTGCGTGAGGAGATCTGGCCAAGTTCTGCACTGGCT  
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTACGTGCTGAGCTGCTCAGGTCTTTCTTTATGTACGGAGACCAGCTTTCAAGAAGCAGGCTCTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAGCATTGG  
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

Fig. 11T



AATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGA  
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D  
CGGGCTGCGGCCGATTGTGAACATGGACTACGTGCTGGGAGCCAGAACGTTCCGAGAGAAAAGAGGGCCGAGCGTCTACCTCGAGGGTGAAGGCAGTGTTCAGCGTCTCAACTACGA  
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E  
GCGGGCGCGGCCCGCCGCTCTGCTGGGCGCTGTGCTGGGCTGGACGATATCCAGGGCCTGGCGACCTTCGTGCTGCGTGTGCGGGCCAGGACCGCCGCTGAGCTGTACTT  
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F  
TGTC AAG GACAGGCTCAGGAGGTGCATGCCAGCATCATCAACCCAGAACACGTACTGCGTGGTGGTATGCCGTGGTCCA  
V K D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q  
GAAGGCCGCCATGGGCAGTCCGCAAGGCCTTCAAGAGCCAGTCTCTACCTTGACAGACCTCCAGCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAGACCAGCCGCTGAGGGA  
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D  
TGCCGTGCTATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTGGCCTTTCGACGTCTTCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGGCAAGTCTACGTCCAGTG  
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C  
CCAGGGGATCCCGAGGGCTCCATCTCTCCACGCTGCTCTGACGCTGTGCTACGGCGACATGGAGAACAGCTGTTTCCGGGGATTCCGGCGGACGGGCTGCTCCTGCGTTTGGTGA  
Q G I P Q G S I L S T L L C S L C Y G D M E N K L F A G I R R D G L L L R L V D  
TGATTTCTGTGGTGACACCTCACCTCACCCACGCGAAAACCTTCTCAGGACCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACCTGCGGAAGACAGTGGTGAACCTCCC  
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P  
TGTAAGACGAGGCCCTGGGTGGCAGGCTTTTGTTCAGATGCCGGCCACGGCTATTCCCTGGTGGGCTGCTGCTGGATACCCGGACCTGGAGGTGCAGAGCCGACTACTCCAG  
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S S  
CTATGCCCGGACCTCCATCAGAGCCAGTCTACCTTCAACCGCGGCTTCAAGGTGGGAGGAACATGCGTCGAAACTCTTTGGGGTCTTGGGCTGAAGTGTACAGCCTGTTTCTGGA  
Y A R T S I R A S L T F N R G F K A G R N M R R K L F G V L R L K C H S L F L D  
TTTGCAGGTGAACAGCCTCCAGAGGTGTGCACCAACATCTACAAGATCCTCCTGCTGAGGCGTACAGGTTTACGCATGTGTGCTGAGCTCCCATTTTCATCAGCAAGTTTGAAGAA  
L Q V N S L Q T V C T N I Y K I L L L Q A Y R F H A C V L Q L P F H Q Q V W K N  
CCCCACATTTTCTGCGGTGCTCTGACACGGCCTCCCTGCTGCTACTCCATCCTGAAAGCCAAGAACGAGGGATGTGCTGGGGGCCAAGGGCGCCGCGGCTCTGCCCTCCGA  
P T F F L R V I S D T A S L C Y S I L K A K N A E

CCGAAGAAAACATTTCTGCTGACTCCTGCGGTGCTTGGGT  
E E N I L V V T P A V L G S

GGGACAGCCAGAGATGGAGCCACCCGACGCTCGGGTGTGGGAGCTTTCCGGTGTCTCTGGGAGGGAGTTGGGCTGGGCTGTGACTCCTCAGCCTCTGTTTTCCCCCAG  
G Q P E M E P P R R P S G V G S F P V S P G R G V G L G L \*

Fig. 11U



# Truncated telomerase (ver. 2)

ATGCCGCGCGCTCCCGCTGCCAGCGGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGCCACGTTCCGTG  
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGGCGCTGGGGCCCCAGGGCTGGCGCTGGTGACGCGCGGGACCGCGGGCTTTCCGCGCTGGTGGCCAGTGCCTGGTGTGGTGCCTGGGACGACGGCGCCCCCGCGCG  
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

GGCTCCCCGGGGTGGCGTCCGGCTGGGGTTGAGGGCGCGCGGGGGAACAGCGACATGCGGAGAGCAGCGCAGGGGACTCAGGGCGCTCCCCCGCAGGTG  
G L P G V G V R L G L R A A G G N Q R H A E S S A G D S G R F P R R  
A S P G S A S G W G \* G R P G G T S D M R R A A Q A T O G A S P A G  
P P R G R R P A G V E G G R G E P A T C G E Q R R R L R A L P P Q V

CCCCCTCTCCGCGAGGTGCTGCTGCTGAAGGAGCTGGTGGCCCGAGTGTGACAGGCTGTGCGAGCGCGGGCGGAAGACGTGCTGGCTTCGGCTTCGCGTGTGACGGGGCCCCG  
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCGAGGGCTTACCACAGCGTGGCGAGTACCTGCCCAACAGGTGACCGACGCACTGCGGGGAGCGGGGCGTGGGGGCTGCTGCGCGCGGTGGCGACGACGT  
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGTTACCTGCTGGCAGCTGCGCGCTCTTTGCTGGTGGCTCCAGCTGCGCTACAGGTGTGCGGGCGCGCGCTGTACCAGCTCGGGCTGCCACTCAGGCCCGGGCCCCCGC  
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGGACCCGAAGCGTCTGGGATGCGAACGGGCTGGAACCATAGCGTACGGAGGGCGGGGTCCCCCTGGGCTGCCAGCCCCGGGTGCGAGGAGCGGGGGCAGTGC  
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGTCTGCCGTTGCCAAGAGGCCAGGCGTGGCGTGGCCCTGAGCGGAGCGGACCGCGTTGGGCGAGGGTCTGGGCCCCACCGGGCAGGACGCTGGACGAGTGACCG  
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTCTGTGTGTGCTACCTGCCAGACCGCGAAGAAGCCACCTCTTTGGAGGGTGGCTCTCTGGCACGCGCACTCCACCCATCCGTGGGCGGCCAGCACCGGGGGCCCCC  
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGCGGCCACACGTCCTGGGACACGCTTGTCCCCGGTGTACGCGGAGACCAAGCACTTCTCTACTCTCAGGCGACAAGGAGAGCTGCGGCCCCCTCTCTACTCAG  
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTGAGGGCCAGCCTGACTGGCGCTCGGAGGCTCGTGAGACCATTTTCTGGGTCCAGGGCTGGATGCCAGGACTCCCCGAGGTGCCCCGCTGCCCGAGGCTACTGGCA  
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATCGGCCCCCTGTTCTGGAGCTGCTTGGGAACACGCGCAGTGCCCCACGGGGTGTCTCAAGACGCACTGCCGCTGCGAGCTGCGGTACCCAGCAGCGGTGTCTGTGCCG  
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAAGCCCCAGGGCTGTGTGGCGCCCCCGAGGAGGAGACAGACCCCCGCTGCGCTGGTGCAGCTGTCTCCGCGACGACAGCCCCCTGGCAGGTGTACGGCTTCGCTGCGGGCTG  
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCGCGGCTGGTCCCCCAGGCTCTGGGGCTCAGGACACAACGCGCTTCTCAGGAACACCAAGAAGTTATCTCCCTGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCT  
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

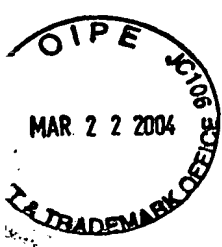
Fig. 11V



GACGTGGAAGATGAGCGTGGGGACTGCGCTTGGCTGCGCAGGAGCCAGGGGTTGGCTGTGTTCCGGCCGAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCTGCACTGGCT  
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L  
GATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTATGTCACGGAGACCACGTTTCAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG  
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G  
AAT--NNN--GACAGTCACCAGGGGGTTGACCGCGGACTGGCGCTCCCAGGGTTGACTATAGGACCAGGTGCCAGGTGCCCTGCAAGTAGAGGGGCTCTCAGAGCGCTCTGGCTGG  
CATGGGTGGACGTGGCCCCGGGCATGGCCTTCTGCGTGTGCTGCCGTGGGTGCCCTGAGCCCTCACTGAGTCGGTGGGGGCTTGTGGCTTCCCGTGAGCTTCCCCCTAGTCTGTTGTCTG  
GCTGAGCAAGCCTCCTGAGGGGCTCTCTATTG...

*Fig. 11W*





# Truncated protein 1 (ver. 2)

ATGCCGCGCGCTCCCGCTGCCGAGCCGTCGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTCTG  
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGGCGCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGGGGACCGGGCGGCTTCCGCGCGCTGGTGGCCAGTGCCTGGTGTGCGTGCCTGGGACGACGGCCGGCCCCCGCCG  
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

GGCCTCCCCGGGGTCCGGCTCCGGCTGGGGTTGAGGGCGGCGGGGGGAACAGCGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCGCGAGGTG  
G L P G V G V R L G L R A A G G N Q R H A E S S A G D S G R F P R R  
A S P G S A S G W G \* G R P G G T S D M R R A A Q A T Q G A S P A G  
P P R G R R P A G V E G G R G E P A T C G E Q R R R L R A L P P Q V

CCCCCTCTCCGCGAGGTGCTGCTGAAGGAGCTGGTGGCCGAGTGTGTCAGAGGCTGTGCGAGCGCGGCGGAAGAACGTGCTGGCCTTCGGCTTCGCGTGTGACGGGGGCCG  
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCGAGGCTTACCACAGCGTGCAGCTACCTGCCCAACAGGTGACCGACGCACTGCGGGGAGCGGGGCGTGGGGGCTGCTGCGCGCGTGGGCGACGACGT  
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTTCACCTGCTGGCAGCTGCCGCTCTTTGTGCTGGTGGCTCCAGCTGCGCTACCAAGGTGTGCGGGCGCGCGTGTACCAGCTCGGCGTGCCTCAGGCCCGGGCCCCG  
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGGACCCGAAGCGCTGCGGATGCGAACGGGCTGGAACCATAGCGTCAAGGAGGCGGGGCTCCCTGGGCTGCCAGCCCCGGGTGCGAGGAGGCGGGGGCAGTGC  
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGTCTGCCGTTGCCAAGAGGCCAGGCGTGGCGCTGCCCCGAGCGGAGCGGACCGCGTGGGCGAGGGTCTGGGCCACCGGGGAGGACGCGTGGACGAGTGACCG  
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGTTTTCTGTGTGTACCTGCCAGACCCGCGAAGAAGCCACTCTTTGGAGGGTGGCTCTCTGGCAGCGCCACTCCACCCATCCGTGGGCGGCCAGCACGCGGGGCCCCC  
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGCGGCCACACGCTCCCTGGGACAGCCTTGTCCCCGGGTGACGCGAGACCAAGCACTTCTCTACTCTCAGGCGACAAGGAGCAGTGGCGCCCTCTCTACTCAG  
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCAGGCGCTGGATGCCAGGGACTCCCCGAGGTTGCCCGCTGCCAGCGCTACTGGCA  
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATGCGGCCCCGTTTCTGAGAGTGTCTGGGAACACGCGCAGTGCCCTACGGGGTGTCTCTAAGACGCACTGCCGCTGCGAGCTGCGGTACCCCGAGCAGCGGTGTGTGTGCCG  
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAAGCCCCAGGGCTCTGTGGCGGGCCCCGAGGAGGAGACAGACCCCGTGCCTGGTGCAGTGTCTCCGCGAGCAGCAGCCCTGGCAGGTGTACGGCTTCGTGGCGGCTG  
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CTGCGCGGCTGGTGGCCCCAGGCTCTGGGGCTCCAGGCACAACGACCGCTTCTCAGGAACCAAGAAGTTCTCTCCCTGGGGAAGCATGCCAAGCTCTCGTGCAGGAGCT  
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

Fig. 11X



GACGTGGAAGATGAGCGTGC GG GACTGCGCTTGGCTGCGCAGGAGCCAGGGGTTGGCTGTGTTCCGGCCGAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCTGCACTGGCT  
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L  
GATGAGTGTGTACGTGCGAGCTGCTCAGGTCTTTCTTTTATGTCAGGAGACCAGGTTTCAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG  
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G  
AATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTGGAAGCAGAGGTCAGGAGCATCGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCAAGCCTGA  
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D

GTGGCTGTGCTTTGGTTAACTTCCTTTTAAACCAGAA  
V A V L W F T F L F N Q K

CGGGCTGCGGCCGATTGTGAACATGGACTACGTGCGGGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTACGCGTGTCAACTACGA  
G L R P I V N M D Y V V G A R T F R R E K R P S V S F R G \*

*Fig. 11Y*



# Truncated protein 2 (ver. 2)

ATGCCGCGCGCTCCCCGCTGCCGAGCGTGGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTCTGT  
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGGCGCTGGGGCCCCAGGGCTGGCGGTGGTGCAGCGCGGGGACCCGCGGCTTTCCGCGCTGGTGGCCAGTGCCTGGTGTGCGTGCCTGGGACGACGCGGCCCGCCCCCGCGC  
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

GGCTCCCCGGGGTCGGCTCCGGCTGGGGTTGAGGGCGCGGGGGGAACAGCGACATGCGGAGAGCAGCGCAGGCGACTCAGGCGCTTCCCCGCGAGGTG  
G L P G V G V R L G L R A A G G N Q R H A E S S A G D S G R F P R R  
A S P G S A S G W G \* G R P G G T S D M R R A A Q A T Q G A S P A G  
P P R G R R P A G V E G G R G E P A T C G E Q R R R L R A L P P Q V

CCCCCTCTCCGCCAGGTGCTCTGCTGAAGGAGCTGGTGGCCGAGTGTGCAGAGGCTGTGCGAGCGCGGCGGAAGACGTGCTGGCTTCGGCTTCGCGCTGCTGGACGGGGCCCG  
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCGAGGCTTACCACCAGCGTGCAGCTACCTGCCAACACGGTGACCGACGCACTGCGGGGAGCGGGGCGTGGGGGCTGCTGCTGCGCGCGTGGGACGACGT  
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGTTACCTGCTGGCAGCTGCGCGCTCTTTGTGCTGGTGGCTCCAGCTGCGCTACCGAGTGTGCGGGCCCGCGTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGGCCCCCGC  
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGGACCCGAAGCGCTGGGATGCGAACGGGCTGGAACCATAGCGTCAGGAGCGCGGGGTCCCCCTGGGCTGCCAGCCCCGGGTGCGAGGAGCGCGGGGCGAGTGC  
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCGAAGTCTGCCGTTGCCAAGAGGCCAGGCGTGGCGCTGCCCCGAGCGGAGCGGACCGCGTGGGCGAGGGGTCTGGGCCCACCGGGCAGGACGCTGGACCGAGTGACCG  
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGTTTCTGTGTGTGTACCTGCCAGACCGCGGAAGACCACTCTTTGGAGGTTGCGCTCTCTGGCACGCGCCACTCCACCCATCCGTGGGCGGCCAGCACCAGCGGGCCCCC  
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGCGCCACCAGTCCCTGGGACACGCTTGTCCCCGGGTACGCCGAGACCAAGCACTTCTCTACTCTCAGGCGACAAGGAGCAGTGGCGCCCTCTTCTACTACG  
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTGAGGCCCCAGCTGACTGGCGCTCGGAGGCTCGTGAGACCATTTCTGGTTCCAGGCGCTGGATGCCAGGACTCCCGCAGGTTGCCCCGCTGCCCGAGCGTACTGGCA  
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATCGGGCCCTGTTTCTGAGCTGCTTGGGAACACGCGAGTGGCCCTACGGGGTGTCTCTAAGACGCACTGCCGCTGCGAGCTGCGGTACCCAGCAGCGGTTGTGTGCCG  
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAAGCCCCAGGCTCTGTGGCGCCCCGAGGAGGAGACAGACCCCCGCTGGCTGGTGCAGTGTCTCGCCAGCAGCAGCCCCCTGGCAGGTGTACGGCTTCTGCGGGCTG  
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCGCGGCTGGTGGCCCCAGGCTCTGGGGTCCAGGCACAACGACCGCTTCTCAGGAACACCAAGAAGTTCTATCTCCCTGGGGAAGCATGCCAAGCTCTCGTGCAGGAGT  
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

Fig. 11Z



GACGTGGAAGATGAGCGTGC GGGACTGCGCTTGGCTGCGCAGGAGCCAGGGGTTGGCTGTGTTCGGCCGAGAGCACCCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCAGTGGCT  
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L  
GATGAGTGTGTACGTGCTCAGCTGCTCAGGTCTTTCTTTATGTCACGGAGACCACGTTTCAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG  
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G  
AATCAGACAGCACTTGAAGAGGGTGAGCTGCGGGAGCTGTGGAAGCAGAGGTGAGGAGCATCGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGA  
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D  
CGGGCTGCGCCGATTGTGAACATGGACTACGTGCTGGGAGCCAGAAGCTTCCGAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTACAGCTGCTCAACTACGA  
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E  
CGGGCGCGGCCCGGCCCTCCTGGGCGCTCTGTGCTGGGCTGGACGATATCCAGGGCTGGGCGACCTTCGTGCTGCGTGTGCGGGCCAGGACCCGCGCCTGAGCTGTACTT  
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F  
TGTAAGGTGGATGTGACGGGCGGTACGACACCATCCCCAGGACAGGCTCAGGAGGTGATCGCCAGCATCATCAACCCAGAACACGTACTGCGTGGCTGGTATGCCGTGGTCCA  
V K V D V T G A Y D T I P Q D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q  
GAAGGCCGCCCATGGGACGTCCGCAAGGCCTTCAAGAGCCAC  
K A A H G H V R K A F K S H

GTCTACGTCCAGTG  
V L R P V

CCAGGGGATCCCGAGGGCTCCATCCTCTCCAGCTGCTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGGGGGATTGCGGGGACGGGCTGCTCCTGCTTGGTGA  
P G D P A G L H P L H A A L Q P V L R R H G E Q A V C G D S A G R A A P A F G G  
TGATTTCTGTTGGTGACACCTCACCTACCCACGCGAAAACCTTCTCAGGACCTGGTCCGAGGTGTCCTGAGTATGGCTGCGTGGTGAACCTGCGGAAGACAGTGGTGAACCTCCC  
★

*Fig. 11AA*



Reference protein (ver. 2)

ATGCCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAG 60  
MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 20

GTGCTGCCGCTGGCCACGTTCTGTCGGGCGCTGGGGCCCCAGGGCTGGCGGCTGGTGCAG 120  
ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln 40

CGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCAGTGCCTGGTGTGCGTGCCCTGG 180  
ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp 60

GACGCACGGCCGCCCCCGCCGCCCTCCTTCCGCCAGGTG  
AspAlaArgProProProAlaAlaProSerPheArgGlnVal

GGCCTCCCCGGGGTCGGCGTCCGGCTGGGGTTGAGGGCGGCCGGGGGAACCAGCGACATGCGGAG  
G L P G V G V R L G L R A A G G N Q R H A E  
A S P G S A S G W G \* G R P G G T S D M R R  
P P R G R R P A G V E G G R G E P A T C G E

AGCAGCGCAGGCGACTCAGGGCGCTTCCCCCGCAGGTG  
S S A G D S G R F P R R  
A A Q A T Q G A S P A G  
Q R R R L R A L P P Q V

TCCTGCCTGAAGGAGCTG 240  
SerCysLeuLysGluLeu 80

GTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGCGCGAAGAACGTGCTGGCCTTCGGC 300  
ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly 100

TTCGCGCTGCTGGA<sup>~</sup>GGGGCCCGCGGGGGCCCCCCCCGAGGCCTTACCACCAGCGTGCGC 360  
PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg 120

AGCTACCTGCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTG 420  
SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu 140

TTGCGCCGCGTGGGCGACGACGTGCTGGTTACCTGCTGGCACGCTGCGCGCTCTTTGTG 480  
LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160

CTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCGCTGTACCAGCTCGGCGCT 540  
LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180

GCCACTCAGGCCCGCCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAA 600  
AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 200

*Fig. 11AB*



|  |      |
|--|------|
| CGGACCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGT | 660  |
| ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly | 220  |
| <br>   |      |
| GCGAGGAGGCGCGGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCCAAGAGGCCAGGCGT   | 720  |
| AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg | 240  |
| <br>   |      |
| GGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGTCTGGGCCACCCGGGC    | 780  |
| GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly | 260  |
| <br>   |      |
| AGGACGCGTGGACCGAGTGACCGTGGTTTCTGTGTGGTGTACCTGCCAGACCCGCCGAA  | 840  |
| ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu | 280  |
| <br>   |      |
| GAAGCCACCTCTTTGGAGGGTGCCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGC  | 900  |
| GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly | 300  |
| <br>   |      |
| CGCCAGCACACGCGGGCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCCT   | 960  |
| ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro | 320  |
| <br>   |      |
| TGTCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAG  | 1020 |
| CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln | 340  |
| <br>   |      |
| CTGCGGCCCTCCTTCTACTCAGCTCTCTGAGGCCAGCCTGACTGGCGCTCGGAGGCTC   | 1080 |
| LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu | 360  |
| <br>   |      |
| GTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGAGGTTGCCC  | 1140 |
| ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro | 380  |
| <br>   |      |
| CGCCTGCCCCAGCGCTACTGGCAAATGCGGCCCTGTTTCTGGAGCTGCTTGGGAACCAC  | 1200 |
| ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis | 400  |
| <br>   |      |
| GCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCCGTGCGAGCTGCGGTCACC | 1260 |
| AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr | 420  |
| <br>   |      |
| CCAGCAGCCGGTGTCTGTGCCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCCGAGGAG | 1320 |
| ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu | 440  |
| <br>   |      |
| GAGGACACAGACCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCTGGCAG   | 1380 |
| GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln | 460  |
| <br>   |      |
| GTGTACGGCTTCGTGCGGGCCTGCCTGCGCCGGTGGTGCCCCAGGCCTCTGGGGCTCC   | 1440 |
| ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer | 480  |
| <br>   |      |
| AGGCACAACGAACGCCGTTCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCAT   | 1500 |
| ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis | 500  |
| <br>   |      |
| GCCAAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGGCTGCGCTTGCTG  | 1560 |
| AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu | 520  |

*Fig. 11AC*



|  |      |
|--|------|
| CGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGAGAGCACCGTCTGCGTGAGGAGATC  | 1620 |
| ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle | 540  |
| CTGGCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGAGCTGCTCAGGTCTTTC    | 1680 |
| LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe | 560  |
| TTTTATGTCACGGAGACCAGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTC  | 1740 |
| PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal | 580  |
| TGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAG | 1800 |
| TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu | 600  |
| CTGTGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGA  | 1860 |
| LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg | 620  |
| CTCCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTG | 1920 |
| LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal | 640  |
| GGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCA | 1980 |
| GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla | 660  |
| CTGTTACAGCTGCTCAACTACGAGCGGGCGCGGCCCGCCCTCCTGGGCGCCTCTGTG    | 2040 |
| LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal | 680  |
| CTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAG | 2100 |
| LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln | 700  |
| GACCCGCCGCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATC  | 2160 |
| AspProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle | 720  |
| CCCCAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCAGAACACGTACTGC  | 2220 |
| ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys | 740  |
| GTGCGTCGGTATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAG | 2280 |
| ValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys | 760  |
| AGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTG | 2340 |
| SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu | 780  |
| CAGGAGACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAG | 2400 |
| GlnGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeuAsnGlu | 800  |
| GCCAGCAGTGGCCTCTTCGACGTCTTCTACGCTTCATGTGCCACCACGCCGTGCGCATC  | 2460 |
| AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle | 820  |
| AGGGGCAAGTCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTG  | 2520 |
| ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu | 840  |

*Fig. 11AD*



|   |      |
|---|------|
| CTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTTCGGCGGGAC | 2580 |
| LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp  | 860  |
| GGGCTGCTCCTGCGTTTGGTGGATGATTTCTTGTGGTGACACCTCACCTCACCCACGCG   | 2640 |
| GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla  | 880  |
| AAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACCTG  | 2700 |
| LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu  | 900  |
| CGGAAGACAGTGGTGAACCTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGT   | 2760 |
| ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal  | 920  |
| CAGATGCCGGCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTG   | 2820 |
| GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeu  | 940  |
| GAGGTGCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTC  | 2880 |
| GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe  | 960  |
| AACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGAAACTCTTTGGGGTCTTGCGGCTG   | 2940 |
| AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu  | 980  |
| AAGTGTACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAAC   | 3000 |
| LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn  | 1000 |
| ATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCA  | 3060 |
| IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro  | 1020 |
| TTTCATCAGCAAGTTTGAAGAACCCACATTTTTCTGCGCGTCATCTCTGACACGGCC     | 3120 |
| PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAla  | 1040 |
| TCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGC  | 3180 |
| SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly  | 1060 |
| GCCGCCGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCTGCTC   | 3240 |
| AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu  | 1080 |
| AAGCTGACTCGACACCGTGTACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAG   | 3300 |
| LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln  | 1100 |
| ACGCAGCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGCCCGCAGCCAAC  | 3360 |
| ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAlaAsn  | 1120 |
| CCGGCACTGCCCTCAGACTTCAAGACCATCCTGGAC                          | 3420 |
| ProAlaLeuProSerAspPheLysThrIleLeuAsp                          | 1132 |

*Fig. 11AE*





# Truncated protein 3 (ver. 2)

ATGCCGCGCGCTCCCGCTGCCGAGCGGTGCGCTCCCTGCTGCCGAGCCACTACCGGAGGTGCTGCCGTGGCCACGTTCTGTG  
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGGCGCTGGGGCCCCAGGGCTGGCGGTGGTGCAGCGGGGACCGCGGCTTTCCGCGCGCTGGTGGCCAGTGCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCGCCG  
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

GGCTCCCGGGGTGCGGTCCGGCTGGGGTTGAGGGCGGGGGGAACAGCGACATGCGGAGAGCAGCGAGGCGACTCAGGGCGCTTCCCCCGAGGTG  
G L P G V G V R L G L R A A G G N Q R H A E S S A G D S G R F P R R  
A S P G S A S G W G \* G R P G G T S D M R R A A Q A T Q G A S P A G  
P P R G R R P A G V E G G R G E P A T C G E Q R R R L R A L P P Q V

CCCCCTTCCGCGAGGTGCTGCTGAAGGAGCTGGTGGCCGAGTGTGCAGAGGCTGTGCCGAGCGGGCGGAAGAAGTGTGGCTTCCGGCTTCCGCGTGTGGACGGGGCCG  
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCGAGGCTTACCACAGCGTGGCGAGTACCTGCCAACACGGTGACCGACGCACTGCCGGGGAGCGGGGCTGGGGGCTGCTGCTGCCCGCGTGGGCGACGACGT  
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTTACCTGCTGGCAGCTGCGCGCTTTTGTGCTGGTGGCTCCAGCTGCGCTACCAGGTGTGCGGGCGCCGCTGTACCAGTCTGGCGCTGCCACTCAGGCCCGGGCCCCCGC  
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGAGCCCGAAGGCGTCTGGGATGCCAAGGGCTGGAACATAGCGTCAGGGAGGGCGGGTCCCCCTGGGCTGCCAGCCCCGGTGCGAGGAGCGGGGGCAGTGC  
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCGAAGTCTGCCGTTGCCAAGAGGCCAGGCGTGGCGCTGCCCTGAGCGGAGCGGACGCCGTTGGGCAAGGGTCTGGGCCACCCGGGAGGACGCTGGACCGAGTGACCG  
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTCTGTGTGTGCTACCTGCCAGACCCGCCAAGAAGCCACCTCTTTGGAGGGTGGCTCTCTGGCAGCGCCACTCCACCCATCCGTGGGCGCCAGCACCAGCGGGCCCCC  
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGCGGCCACACGTCCTGGGACAGCCTTGTCCCCGGTGTACGCGGAGACCAAGCACTTCTCTACTCTCAGGCGACAAGGAGCAGTGGCGCCCTCTCTCTACTCAG  
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGAGACCATTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGAGGTTGCCCGCTGCCCGAGCCTACTGGCA  
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATGCGGCCCTGTTTCTGGAGCTGCTTGGGAACACGCGCAGTGCCCTACGGGGTGTCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTACCCGAGCAGCGGGTGTGTGCCCCG  
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAAGCCCCAGGGCTCTGTGGCGCCCCGAGGAGGAGACAGACCCCGTCCGCTGGTGCAGCTGCTCCGCCAGCAGCAGCCCTGGCAGGTGTACGGCTTCTGTGCGGGCTG  
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCGCGGGTGGTGGCCCCAGGCTCTGGGGCTCCAGGCACAACGACCGCGCTTCTCAGGAACCAAGAAGTTATCTCCCTGGGAAGCATGCCAAGCTCTCGTGCAGGAGT  
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

Fig. 11AF



GACGTGGAAGATGAGCGTGGGGACTGCGCTTGGCTGCCGAGGAGCCAGGGGTTGGCTGTGTTCCGGCCGAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCCTGGCT  
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTGACGTCGTCGAGCTGCTCAGGTCTTTCTTTATGTACGGAGACCAGCTTTCAAAGAAGAGGCTCTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG  
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

AATCAGACAGCACTTGAAGAGGGTGACGCTGCGGGAGCTGTGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGA  
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D

CGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAAGCTTCCGAGAGAAAGAGGGCCGAGCGTCTACCTCGAGGGTGAAGGCACTGTTGAGCGTCTCAACTACGA  
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E

GGGGCGCGCGCCCGGCTCTGGGCGCTGTGCTGGGCTGGAGCATATCCAGGGCTGGCGACCTTCGTGCTGCGTGTGGGGCCAGGACCCGCCGCTGAGCTGTACTT  
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F

TGTAAGGTGGATGTGACGGGCGGTACGACACCATCCCCAGGACAGGCTCAGGAGGTATCGGCAGCATCATCAACCCAGAACACGTAAGTGTGCGTGGTATGCGGTGGTCCA  
V K V D V T G A Y D T I P Q D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q

GAAGGCGGCCATGGGCAGTCCGCAAGGCCCTCAAGAGCCAGCTCTACCTTGACAGACTCCAGCGTACATGCGACAGTTGCTGGCTCACCTGCAGGAGACCAGCCGCTGAGGGA  
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D

TGCCGTCGTATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTGGCTCTTCGACGTCTTCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGCAAGTCTACGTCCAGTG  
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C

CCAGGGGATCCCGAGGGCTCCATCTCTCCACGCTGCTCTGCAGCCTGTGCTACGGCAGATGGAGAACAAGCTGTTTGGGGGATTGCGGGGACGGGCTGCTCCTGCGTTTGGTGA  
Q G I P Q G S I L S T L L C S L C Y G D M E N K L F A G I R R D G L L L R L V D

TGATTTCTGTTGGTGACACCTCACCTCACCCACGCCAAAACCTTCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAAGTTCGGAAGACAGTGGTGAAGTTCCTCC  
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P

TGTAGAAGACGAGGCCCTGGGTGGCAGGCTTTTGTTCAGATGCCGGCCACGGCTATTCCCTGGTGGGCTGCTGCTGGATACCCGAGCCCTGGAGGTGCAGAGCGACTACTCCAG  
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S R

GTGAGCGCACCTGGCCGGAAGTGAGCCTGTGCCGGCTGGGGCAGGTGCTGCTGACGGGCCGTGGCTCCACCTCTGCTTCCGTGTGGGGCAGGCGACTGCCAATCCCAAAGGGTCAGA  
\*

TGCCACAGGGTGCCCTCGTCCCATCTGGGGCTGAGCACAATGCATCTTTCTGTGGGAGTGAGGGTGCCCTCACACGGGAGCAGTTTTCTGTGCTATTTTGGTAA...

*Fig. 11AG*



# Altered C-terminus protein (ver. 2)

ATGCCGCGCGCTCCCCGCTGCCAGCCGCTGCGCTCCCTGCTGCCAGCCACTACCGCGAGGTGCTGCCGTGCCACGTTCTG  
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGGCGCTGGGGCCCCAGGGCTGGCGGCTGGTGACGCGGGGACCGCGGCTTTCCGCGCGCTGGTGCCAGTGCTGGTGCGTGCCCTGGGACGACGGCGCCCCCGCGC  
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

GGCCTCCCCGGGTGCGGCTCCGGCTGGGGTTGAGGGCGGGGGGAACAGCGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTCCCCCGCAGGTG  
G L P G V G V R L G L R A A G G N Q R H A E S S A G D S G R F P R R  
A S P G S A S G W G \* G R P G G T S D M R R A A Q A T Q G A S P A G  
P P R G R R P A G V E G G R G E P A T C G E Q R R R L R A L P P Q V

CCCCCTCTCCGCGAGGTGCTGCTGAAGGAGCTGGTGCCCGAGTGCTGCAGAGGCTGTGCGAGCGGGCGGAAGAAGTGCTGGCTTCGGCTTCGCGCTGCTGGACGGGGCGG  
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCGAGGCTTACCACAGCGTGCGCAGCTACCTGCCAACACGGTGACCGACGCACTGCGGGGAGCGGGGCTGGGGGCTGCTGCTGCCCGCGTGCGGCGACGAGCT  
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTTACCTGCTGGCAGCTGCGCGCTTTTGCTGGTGGCTCCAGCTGCGCTACCAGGTGTGCGGGCGCGGCTGTACCAGCTCGGCGCTGCCACTCAGGCCGGGGCCCCCGC  
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGAGCCCCGAAGCGCTGGGATGCGAACGGGCTGGAACCATAGCGTCAGGGAGGCGGGGCTCCCCCTGGGCTGCCAGCCCCGGGTGCGAGGAGGCGGGGGCAGTGC  
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCGAAGTCTGCCGTTGCCAAGAGGCGGAGGCTGCGGCTGCCCTGAGCGGAGCGGACCGCGTTGGGCAAGGGTCTGGGGCCACCGGGCAGGACGCTGGACCGAGTGACCG  
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTCTGTGGTGTACCTGCCAGACCCCGGAAGGCCACCTCTTTGGAGGGTGCCTCTGTGCGACGCGCACTCCACCCATCCGTTGGGCGCCAGCACCACGCGGGCCCCC  
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGCGGCCACCGCTCCCTGGGACACGCTTGTCCCCGGGTACGCGGAGACCAAGCACTTCTCTACTCTCAGGCGACAAGGAGCAGCTGCGGCGCTCTCTACTCAG  
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTGAGGCGCCAGCTGACTGGCGCTCGGAGGCTCGTGAGACCATCTTTCTGGGTTCCAGGCGCTGGATGCCAGGGACTCCCCGAGGTTGCCCCGCTCCCCAGCGCTACTGGCA  
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATGCGGCCCCGTTTCTGGAGCTGCTTGGGAACACGCGCAGTGCCCCACGGGGTGTCTCTCAAGACGCACTGCGCGTGGAGCTGCGGTACCCAGCAGCGGCTGTCTGCGCGC  
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAAGCCCCAGGGCTCTGTGGCGGCCCCGAGGAGGAGACAGACCCCCGTCGCTGGTGACGTGCTCCGCGACGACAGCGCCCTGGCAGGTGTACGCTCTGTCGGGCGCTG  
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCGCGGCTGGTGCCCCAGGCTCTGGGCTCCAGGCACAACGAACCGCGCTTCTCAGGAACACCAAGAAGTTCTCTCCCTGGGAAGCATGCCAAGCTCTGCTGCGGAGGT  
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

Fig. 11AH



GACGTGGAAGATGAGCGTGGGACTGCGCTTGGCTGCGCAGGAGCCAGGGGTGGCTGTGTTCCGGCCGAGAGCACCCTGCGTGAGGAGATCTGGCCAAGTTCCTGCACTGGCT  
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTGACGTGCTGAGCTGCTCAGGTCTTTCTTTATGTACGGAGACCACGTTTCAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTG  
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

AATCAGACAGCACTTGAAGAGGGTGACGTGCGGAGCTGTGGAAGCAGAGGTACGGCAGCATCGGGAAGCCAGGCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGA  
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D

CGGGCTGCGGCCGATTGTGAACATGGACTACGTGCTGGGAGCCAGAAGCTTCCGACAGAAAAGAGGGCCGAGCGTCTACCTCGAGGGTGAAGGCACTGTTACGGCTGCTCAACTACGA  
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E

GCGGGCGCGGCCGCCGCTCTGGGCGCTCTGTGCTGGGCTGGAGCATATCCAGGGCTGGCGACCTTCGTGCTGCGTGTGCGGGCCAGGACCCGCGCTGAGCTGTACTT  
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F

TGTCAAGGTGGATGTGACGGGCGGTACGACACCATCCCCAGGACAGGCTACGGAGGTACATCGCCAGCATCATCAAAACCCAGAACACGTACTGCGTGGTGGTATGCCGTGGTCCA  
V K V D V T G A Y D T I P Q D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q

GAAGGCCGCCATGGGACGTCCGCAAGGCCCTCAAGAGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAGACCAGCCCGCTGAGGGA  
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D

TGCCGTGTCATGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTGGCTCTTGACGTCTTCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGGCAAGTCTACGTCCAGTG  
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C

CCAGGGGATCCCGAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCCTGTGTACGGGACATGGAGAACAAGCTGTTTGGGGGATTGCGGGGACGGGCTGCTCCTGCTTTGGTGA  
Q G I P Q G S I L S T L L C S L C Y G D M E N K L F A G I R R D G L L L R L V D

TGATTTCTGTTGGTGACACCTCACCTCACCCACGCAAAACCTTCTCAGGACCCTGGTCCGAGGTGCTCCTGAGTATGGCTGCGTGGTGAACCTTGGGAAGACAGTGGTGAACCTCCC  
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P

TGTAGAAGACGAGGCCCTGGGTGGCAGGCTTTTGTTCAGATGCCGGGCCACGGCCTATTCCCTGGTGGCGCTGCTGCTGGATACCCGGACCTGGAGGTGCAGAGGCACTACTCCAG  
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S S

CTATGCCCGACCTCCATCAGAGCAGTCTCACCTTCAACCGGGCTTCAAGGTGGGAGGAACATGCGTCGAAACTCTTTGGGGTCTTGGCGTGAAGTGTACAGCCTGTTTCTGGA  
Y A R T S I R A S L T F N R G F K A G R N M R R K L F G V L R L K C H S L F L D

TTTGAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTACAAGATCCTCTGCTGCAGGCGTACAGGTTTACGCATGTGTGCTGCAGCTCCCATTTTCATCAGCAAGTTTGAAGAA  
L Q V N S L Q T V C T N I Y K I L L L Q A Y R F H A C V L Q L P F H Q Q V W K N

CCCCACATTTTCTGCGGTCTCTGACACGGCTCCTCTGCTACTCCATCCTGAAAGCCAAGAAGCAGGAGTGTGCTGGGGCCAAGGGCGCCGCGGCCCTCTGCCCTCCGA  
P T F F L R V I S D T A S L C Y S I L K A K N A E

CCGAAGAAAACATTTCTGCTGACTCCTGCGGTGCTTGGGT  
E E N I L V V T P A V L G S

GGGACAGCCAGAGATGGAGCCACCCCGACACCGTGGGTGTGGGAGCTTTCCGGTGTCTCTGGGAGGGAGTTGGGTGGGCTGTGACTCCTCAGCCTCTGTTTTCCCCAG  
G Q P E M E P P R R P S G V G S F P V S P G R G V G L G L \*

Fig. 11AI



Protein that lacks motif A (ver. 2)

ATGCCGCGCGCTCCCGCTGCCGAGCGTGGCTCCCTGCTGCGCAGCCACTACCGCAGGTGCTGCCGCTGGCCACGTTCTGT  
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGGCGCTGGGGCCCCAGGGCTGGCGGCTGGTGACGCGCGGGGACCGCGGCTTCCGCGCGCTGGTGGCCAGTGCCTGGTGTGCGTGCCTGGGACGCACGGCCGCCCCCGCGC  
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

GGCCTCCCCGGGTGCGCGTCCGGCTGGGGTTGAGGGCGCGCGGGGGAACAGCGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCCCGCAGGTG  
G L P G V G V R L G L R A A G G N Q R H A E S S A G D S G R F P R R  
A S P G S A S G W G \* G R P G G T S D M R R A A Q A T Q G A S P A G  
P P R G R R P A G V E G G R G E P A T C G E Q R R R L R A L P P Q V

CCCCCTCTCCGCCAGGTGCTGCTGAAGGAGCTGGTGGCCGAGTGTGACAGGCTGTGCGAGCGCGGCGGAAGAACGTGCTGGCTTCGGCTTCGCGCTGCTGGACGGGGCCG  
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCGAGGCTTCACCACAGCGTGGCGAGCTACCTGCCCAACACGCTGACCGACGCACTGCGGGGAGCGGGGCGTGGGGGCTGCTGCTGCGCCGCTGGGCGACGAGCT  
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGTTACCTGCTGGCAGCTGCGCGCTTTTGTGCTGGTGGCTCCAGCTGCGCTACAGGTGTGCGGGCCCGCGTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGGCCCCCGC  
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGGACCCGAAGGCGTCTGGGATCGGAACGGGCTGGAACATAGCGTCAGGGAGGCGGGGTCCCCCTGGGCTGCCAGCCCCGGGTGCGAGGAGGCGGGGGCAGTGC  
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCGAAGTCTGCCGTTGCCAAGAGGCGCAGGCGTGGCGCTGCCCTGAGCGGAGCGAGCGCCGTGGGCGAGGGGCTCTGGGCCACCCGGGCGAGCGGTGGACGAGTGACCG  
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTTCTGTGGTGTACCTGCCAGACCCGCGGAAGAAGCCACCTCTTTGAGGGGTGCGCTCTCTGGCACGGCCACTCCACCCATCCGTGGGCGCCAGCACACGCGGGCCCCC  
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGCGGCCACCAGTCCCTGGGACACGCTTGTCCCCGGGTACGCCGAGACCAAGCACTTCTCTACTCTCAGGCGACAAGGAGCAGCTGCGGCCCTCTCTCTACTCAG  
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTCTGAGGCCAGCCTGACTGGCGCTCGGAGGCTCGTGAGACCATCTTTCTGGGTTCAGGCCCTGGATGCCAGGGACTCCCGCAGGTTGCCCCGCTGCCCCAGCGCTACTGGCA  
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATCGGGCCCTGTTTCTGAGCTGCTTGGGAACACGCGCAGTGCCCTACGGGGTGTCTCTAAGACGCACTGCCGCTGCGAGCTGCGGTACCCAGCAGCGGCTGTCTGTGCCCCG  
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAAGCCCCAGGCTCTGTGGCGGCCCCGAGGAGGAGACAGACCCCGCTCGCTGGTGCAGTGTCTCGCCAGCACAGCAGCCCTGGCAGGTGTACGGCTTCTGTGGGGCGCTG  
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCGCGGCTGGTGGCCCCAGGCTCTGGGGCTCCAGGCACAACGAACGCGCTTCTCAGGAACCAAGAAGTTCATCTCCTGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCT  
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

Fig. 11AJ



GACGTGGAAGATGAGCGTGGGACTGCGCTTGGCTGCGCAGGAGCCAGGGGTGGCTGTGTTCCGGCCGAGAGCACCCTGCGTGAGGAGATCTGGCCAAGTTCTGCACTGGCT  
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTGTACGTCGTGAGCTGCTCAGGCTTTTCTTTATGTACGGAGACCAGTTTCAAAGAAGAGGCTCTTTTCTACCGAAGAGTGTCTGGAGCAAGTTGCAAGCATTGG  
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

AATCAGACAGCACTTGAAGAGGGTGAGCTGCGGAGCTGTGGAAGCAGAGGTGAGCAGCATCGGAAGCCAGGCCCGCTGCTGACGTCCAGACTCCGCTTCATCCCAAGCCTGA  
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D

CGGGCTCGGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTGAGCGTGTCAACTACGA  
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E

GCGGGCGGGCCCGGCTCTCTGGGCGCTGTGTCTGGGCTGGACGATATCCAGGGCTGGCGCACCTTCGTGCTGCGTGTGGGGCCAGGACCCCGGCTGAGCTGTACTT  
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F

TGTCAGG  
V K

GACAGGCTCAGGAGGTATCGCCAGCATCATAAACCCAGAACACGTACTGCGTGGTGGTATGCCGTGGTCCA  
D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q

GAAAGCCGCCCATGGGCAGCTCCGCAAGGCTTCAAGAGCCAGCTCTACCTTGACAGACCTCCAGCCGTACATGCCAGTTCGTGGCTCACCTGAGGAGACACGCCGCTGAGGGA  
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D

TGCCGTGTCATCGAGCAGAGCTCTCTCCCTGAATGAGGCCAGCAGTGGCTCTTGACGCTCTCTACGCTTCATGTGCCACCAGCCGTGCCATCAGGGGCAAGTCTACGTCCAGTG  
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C

CCAGGGATCCCGAGGGCTCCATCTCTCCAGCTGCTGTGACGCTGTGCTACGGGACATGGAGAACAAGCTGTTTGGGGGATTCGGGGGAGGGGTGCTCTCTGCGTTTGGTGA  
Q G I P Q G S I L S T L L C S L C Y G D M E N K L F A G I R R D G L L L R L V D

TGATTCTGTGTTGGTGACACCTCACCTCACCCACGCAAAACCTTCTCAGGACCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACCTGCGGAAGACAGTGGTGAACCTCC  
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P

TGTAGAAGACGAGGCCCTGGGTGGCAGGCTTTTGTTCAGATGCCGGCCACGGCTATTCCTCTGGTGGGCTGCTGCTGGATACCCGAGCCCTGGAGGTGCAGAGCAGTACTCCAG  
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S S

CTATGCCCGGACCTCATCAGAGCCAGTCTCACCTTCAACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTTTGGGGTCTTGGGCTGAAGTGTACAGCCTGTTTCTGGA  
Y A R T S I R A S L T F N R G F K A G R N M R R K L F G V L R L K C H S L F L D

TTTGAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTACAAGATCTCTGCTGACGGGTACAGGTTTACGCAATGTGTGCTGACGTCCCATTTTCATCAGCAAGTTTGAAGAA  
L Q V N S L Q T V C T N I Y K I L L L Q A Y R F H A C V L Q L P F H Q Q V W K N

CCCCACATTTTCTGCGGTCATCTCTGACAGGCTCCCTCTGCTACTCCATCTGAAAGCAAGAAGCAGGGATGTGCTGGGGCCAAAGGGCGCCCGGCTCTGCTCTCCGA  
P T F F L R V I S D T A S L C Y S I L K A K N A G M S L G A K G A A G P L P S E

GGCGGTGAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCTGACTCGACACCGTGTACCTACGTGCCACTCTGGGGTCACTCAGGACAGCCAGAGCAGCTGAGTCGGAAGCTCCC  
A V Q W L C H Q A F L L K L T R H R V T Y V P L L G S L R T A Q T Q L S R K L P

GGGACGACGCTGACTGCCCTGGAGGGCCAGCCAAACCGGCACTGCCCTCAGACTTCAAGACCATCTGGAGTGATGGCCACCCGCCACAGCCAGGCGAGAGCAGACACAGCAGCC  
G T T L T A L E A A A N P A L P S D F K T I L D

Fig. 11AK



CTGTCACGCCGGGCTCTACGTCCAGGGAGGGAGGGGGGCCACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTGGCCGAGGCCTGCATGTCCGGCTGAAGGCT  
GAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCAGGGCCAGCTTTCTCTAC  
CAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCAGATTGCCATTGTTACCCCTCGCCCTGCCCTCTTGGCTTCCACCCACCATCCAGGTGGAGCCCTGAGAA  
GGACCCCTGGGAGCTCTGGGAATTTGGAGTGACCAAGGTGTGCCCTGTACACAGGCGAGGACCTGCACCTGGATGGGGTCCCTGTGGGTCAAATTGGGGGAGGTGCTGTGGGAGTAA  
AATACTGAATATATGAGTTTTTCAGTTTTGA

*Fig. 11AL*



Truncated protein that lacks motif A (ver. 2)

ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCAGGTGCTGCCGCTGGCCACGTTCTGT  
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGGCGCTGGGGCCCCAGGGCTGGCGGCTGGTGACGCGGGGACCCGGCGGCTTCCGCGCGTGGTGGCCAGTGCCGTGGTGTGCGTGCCCTGGGACGACGCGCGCCCCCGCCG  
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

GGCCTCCCCGGGTGCGCGTCCGGCTGGGGTTGAGGGCGGCCGGGGGAACAGCGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCCGCAGGTG  
G L P G V G V R L G L R A A G G N Q R H A E S S A G D S G R F P R R  
A S P G S A S G W G \* G R P G G T S D M R R A A Q A T Q G A S P A G  
P P R G R R P A G V E G G R G E P A T C G E Q R R R L R A L P P Q V

CCCTCCTTCCGCCAGGTGCTGCTGAAGGAGCTGGTGGCCGAGTGCTGCAGAGGCTGTGCGAGCGCGCGGGAAGAACGTGCTGGCCTTCGGCTTCCGCGTCTGGACGGGGCCCG  
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCGAGGCTTACCACCAGCGTGGCAGCTACCTGCCCAACACGGTGACCGAGCGACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCTGCGCCGCGTGGGCGACGACGT  
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTTCACCTGCTGGCAGCTGCGCGCTCTTGTGCTGGTGGCTCCAGCTGCGCCTACCAGGTGTGCGGGCCGCGCTGTACCAGCTCGGCGCTGCCACTCAGGCCGGGGCCCCCGC  
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGACCCCGAAGGCGTCTGGGATGCGAACGGGCTGGAACCATAGCGTCAGGGAGGCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAGGAGGCGGGGGCAGTGC  
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGTCTGCCGTTGCCAAGAGGCCAGGCGTGGCGCTGCCCTGAGCCGAGCGGACGCCGTTGGGAGGGGTCTGGGCCACCCGGGAGGACGCGTGACCGAGTGACCG  
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGTTTCTGTGGTGTACCTGCCAGACCCGCCGAAGAAGCCACCTCTTGGAGGGTGGCGTCTCTGGCAGCGCCACTCCACCCATCCGTGGGCGCCAGCACCACGGGGCCCCC  
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGCGGCCACACGCTCCCTGGGACACGCTTGTCCCCGGGTGACGCCAGACCAAGCACTTCTCTACTCTCAGGCGACAAGGAGCAGCTGCGGCCCTCTTCTACTCAG  
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGAGACCATTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCGCAGGTTGCCCCGCTGCCCGAGGCTACTGGCA  
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATGCGGCCCTGTTTCTGGAGCTGCTGGGAACACGCGCAGTGCCCTACGGGGTCTCTCAAGACGCACTGCCGCTGCGAGCTGCGGTACCCAGCAGCGGTGCTGTGCCCC  
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAAGCCCCAGGGCTCTGTGGCGCCCCGAGGAGGAGACAGACCCCCGTGCGCTGGTGCAGTGCTCCGCCAGCACAGCAGCCCTGGCAGGTGTACGGCTCTGTGGGGCTG  
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCGCGGCTGGTGGCCCCAGGCTCTGGGGCTCCAGGCACAACGACCCGCTTCTCAGGAACACCAAGAAGTTCATCTCCCTGGGAAGCATGCCAAGCTCTGCTGCAGGAGCT  
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

Fig. 11AM





GACGTGGAAGATGAGCGTGGGGACTGCGCTTGGCTGCGCAGGAGCCAGGGGTTGGCTGTGTTCCGGCCGAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCACTGGCT  
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTGTACGTGCTGAGCTGCTCAGGTCTTTCTTTTATGTACGAGAGCCACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAGCAAGTGCAGCAAGCATTGG  
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

AATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTGGAAGCAGAGGTGAGGAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGA  
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D

CGGGTGGCGCCGATTGTGAACATGGACTACGTGCTGGGAGCCAGAACGTTCCGAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTGAGCGTCTCAACTACGA  
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E

GCGGGCGCGGCCCGCCCTCTGCTGGGCGCTCTGTGCTGGGCTGGAGCATATCCAGAGGCTGGCGCACCTTCGTGCTGCTGCGGGCCAGGAGCCGCGCCTGAGCTGTACTT  
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F

TGCAAG  
V K

GACAGGCTCACGGAGGTGATCGCCAGCATCATAAACCCAGAACAGTACTGCGTGGTGGTATGCGTGGTCCA  
D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q

GAAGGCCGCCCATGGGACGTCCGCAAGGCCTTCAAGAGCCACGTCTCTACCTTGACAGACCTCCAGCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAGACAGCCCGCTGAGGGA  
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D

TGCGTGTGTCAGGAGAGCTCCTCCTGAATGAGGCCAGTGGCTCTTCAGCTCTTCTACGCTTATGTCACACAGCGCTGCGCATCAGGGGCAAGTCTACGTCCAGTG  
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C

CCAGGGATCCCGAGGGCTCCATCCTCTCCAGCTGCTCTGCAGCTGTGCTACGGGACATGGAGAACAAGCTGTTTGGGGGATTGCGGGGACGGGCTGCTCCTGCGTTTGGTGA  
Q G I P Q G S I L S T L L C S L C Y G D M E N K L F A G I R R D G L L L R L V D

TGATTTCTGTGGTGACACCTCACCTCACCCACGGGAAACCTTCTCAGGACCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACCTGCGGAAGACAGTGGTGAACCTCCC  
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P

TGTAGAAGACAGGCCCTGGGTGGCAGGCTTTTGTTCAGATGCGGGCCACGGGCTATTCCCTGGTGGGCTGCTGCTGGATACCGGACCTGGAGGTGCAGAGCGACTACTCCAG  
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S R

GTGAGCGCACCTGGCCGGAAGTGAGCCTGTGCCCGCTGGGGCAGGTGCTGCTGCAGGGCGTTGCGTCCACCTCTGCTTCCGTGTGGGGCAGGCGACTGCCAATCCCAAGGGTCAGA  
\*

TGCCACAGGGTGGCCCTCGTCCATCTGGGGCTGAGCACAAATGCATCTTTCTGTGGAGTGAGGGTGCCTCACAACGGGAGCAGTTTTCTGTGCTATTTTGGTAA...

Fig. 11AN



Lacks motif A and altered C-terminus (ver. 2)

ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGGAGGTGCTGCCGCTGGCCACGTTCTGT  
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGGCGCTGGGGCCCCAGGGCTGGCGGCTGGTGACGCGGGGACCCGGCGGCTTCCGCGCGTGGTGGCCAGTGCCGTGGTGTGCGTGCCCTGGGACGACGCGCCGCCCGCCGCGC  
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

GGCCTCCCCGGGTGCGCTCGGCTGGGGTTGAGGGCGCGGGGGGAACAGCGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCCCGCAGGTG  
G L P G V G V R L G L R A A G G N Q R H A E S S A G D S G R F P R R  
A S P G S A S G W G \* G R P G G T S D M R R A A Q A T Q G A S P A G  
P P R G R R P A G V E G G R G E P A T C G E Q R R R L R A L P P Q V

CCCCCTCTCCGCCAGGTGTCTGCTGAAGGAGCTGGTGGCCGAGTGCTGCAGAGGCTGTGCGAGCGCGCGCGAAGAACGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCC  
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCGAGGCTTACCACAGCGTGCGCAGCTACCTGCCCAACAGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCTGCGCGCGTGGCGACGACGT  
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTTACCTGCTGGCAGCTGCGCGCTTTGTGCTGGTGGCTCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTGCGCGCTGCCACTCAGGCCCGGGCCCCCGCC  
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGGACCCGAAGGCGTCTGGGATGCGAACGGGCTGGAACCATAGCTCAGGGAGGCGGGGTCCCCCTGGGCTGCCAGCCCCGGGTGCGAGGAGGCGGGGGCAGTGC  
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGTCTGCCGTTGCCAAGAGGCCAGGCGTGGCGCTGCCCTGAGCGGAGCGGACGCCGTTGGGACGGGTCTGGGGCCACCCGGGACGCGTGGACGAGTGACCG  
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTTCTGTGGTGTCACTGCCAGACCCGCGAAGAAGCCACCTTTGGAGGGTGGCGCTCTTGGCAGCGCCACTCCACCCATCCGTGGGCGCCAGCACCACGCGGGCCCCC  
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGCGGCCACCAGTCCCTGGGACAGCCTTGTCGCCCGGTGTACGCCGAGACCAAGCACTTCTCTACTCTCAGGCGACAAGGAGCAGTGCGGCCCTCTCTACTCAG  
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTGTAGGCCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGAGACCATTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGAGGTTGCCCCGCTGCCACGCGTACTGGCA  
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATCGGGCCCTGTTTCTGGAGTGCTTGGGAACACGCGCAGTGCCCCACGGGGTGTCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTACCCACGACGCGGTGTCTGTGCCG  
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAAGCCCAGGGCTCTGTGGCGGCCCCGAGGAGGAGACAGACCCCCGTGCGCTGGTGACGTGCTCGCCAGCACAGCAGCCCTGGCAGGTGTACGGCTTCTGTGGGGCTG  
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCGCGGCTGGTGGCCCGAGGCTCTGGGGCTCCAGGCACAACGACCGGCTTCTCAGGAACCAAGAAGTTCATCTCCCTGGGAAGCATGCCAAGCTCTGCTGCAGGAGCT  
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

Fig. 11AO



GACGTGGAAGATGAGCGTGGGACTGCGCTTGGCTGCCAGGAGCCAGGGTTGGCTGTGTTCCGGCCGAGAGCACCGTCTGCGTGAGGAGATCTGGCCAAGTTCCTGCACTGGCT  
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTGTACGTGCTGAGCTGCTCAGGTCTTTCTTTATGTACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAGCAAGTGCAGCAATTGG  
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

AATCAGACAGCACTTGAAGAGGGTGACGTGCGGGAGCTGTGGAAGCAGAGGTGAGGAGCATCGGGAAGCCAGGCCCGCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGA  
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D

CGGGCTGCGGCCATTGTGAACATGGACTACGTGCTGGGAGCCAGAACGTTCCGAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTGAGCGTCTCAACTACGA  
G L R P I V N M D Y V V G A R T F R E K R A E R L T S R V K A L F S V L N Y E

GCGGGCGCGGCCCGGCTCTGCTGGGCGCTCTGCTGGGCTGGACGATATCCAGAGGCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCAGGACCCGCGCTGAGCTGTACTT  
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F

TGCAAG  
V K

GACAGGCTCACGGAGTGCATGCCAGCATCAAAACCCAGAACACTACTGCGTGGTGGTATGCCGTGGTCCA  
D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q

GAAGGCCGCCCATGGGACGTCCGAAGGCCCTCAAGAGCCAGCTCTACCTTGACAGACCTCCAGCGTACATGCCAGTTCGTGGCTCACCTGCAGGAGACCAGCCCGCTGAGGGA  
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D

TGCGTGTGTCAGGAGAGCTCTCCCTGAATGAGGCCAGTGGCTCTTCAGCTCTTCTACGCTTCATGTGCCACCAGCGGTGCGCATCAGGGCAAGTCTACGTCCAGTG  
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C

CCAGGGATCCCGCAGGGCTCCATCTCTCCAGCTGCTCTGCAGCTGTGCTACGGGACATGGAGAACAGCTGTTTGGGGGATTGCGGGGACGGGCTGCTCTCGCTTTGGTGA  
Q G I P Q G S I L S T L L C S L C Y G D M E N K L F A G I R R D G L L L R L V D

TGATTTCTGTGGTGACACCTCACCTCACCCAGCGAAAACCTTCTCAGGACCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACCTTCCGAAGACAGTGGTGAACCTCCC  
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P

TGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCACGGCTATTCCCTGGTGGGCTGCTGCTGGATACCGGACCTGAGGTGCAGAGCGACTACTCCAG  
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S S

CTATGCCCGACCTCCATCAGAGCCAGTCTCACCTTCAACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTGGGGTCTTGGGCTGAAGTGTACAGCCTGTTTCTGGA  
Y A R T S I R A S L T F N R G F K A G R N M R R K L F G V L R L K C H S L F L D

TTTGCAGGTGAACAGCCTCCAGAGGGTGTGCACCAACATCTACAAGATCTCTGCTGCAGGGTACAGGTTTACGCATGTGTGCTGCAGCTCCCATTTTCATCAGCAAGTTTGAAGAA  
L Q V N S L Q T V C T N I Y K I L L L Q A Y R F H A C V L Q L P F H Q Q V W K N

CCCCACATTTTCTGCGGTGCTCTGTGACAGGGCTCCCTCTGCTACTCCATCTGAAAGCCAAGAACGAGGGATGTGCTGGGGGCCAAGGGCGCCCGGCTCTGCTCTCCGA  
P T F F L R V I S D T A S L C Y S I L K A K N A E

CCGAAGAAAACATTTCTGCTGACTCTGCGGTGCTTGGGT  
E E N I L V V T P A V L G S

GGGACAGCCAGAGATGGAGCCACCCGAGACCGTGGGTGTGGGAGCTTTCCGGTGTCTCTGGGAGGGGAGTTGGGCTGGGCTGTGACTCCTCAGCCTCTGTTTTCCCGAG  
G Q P E M E P P R R P S G V G S F P V S P G R G V G L G L \*

Fig. 11AP

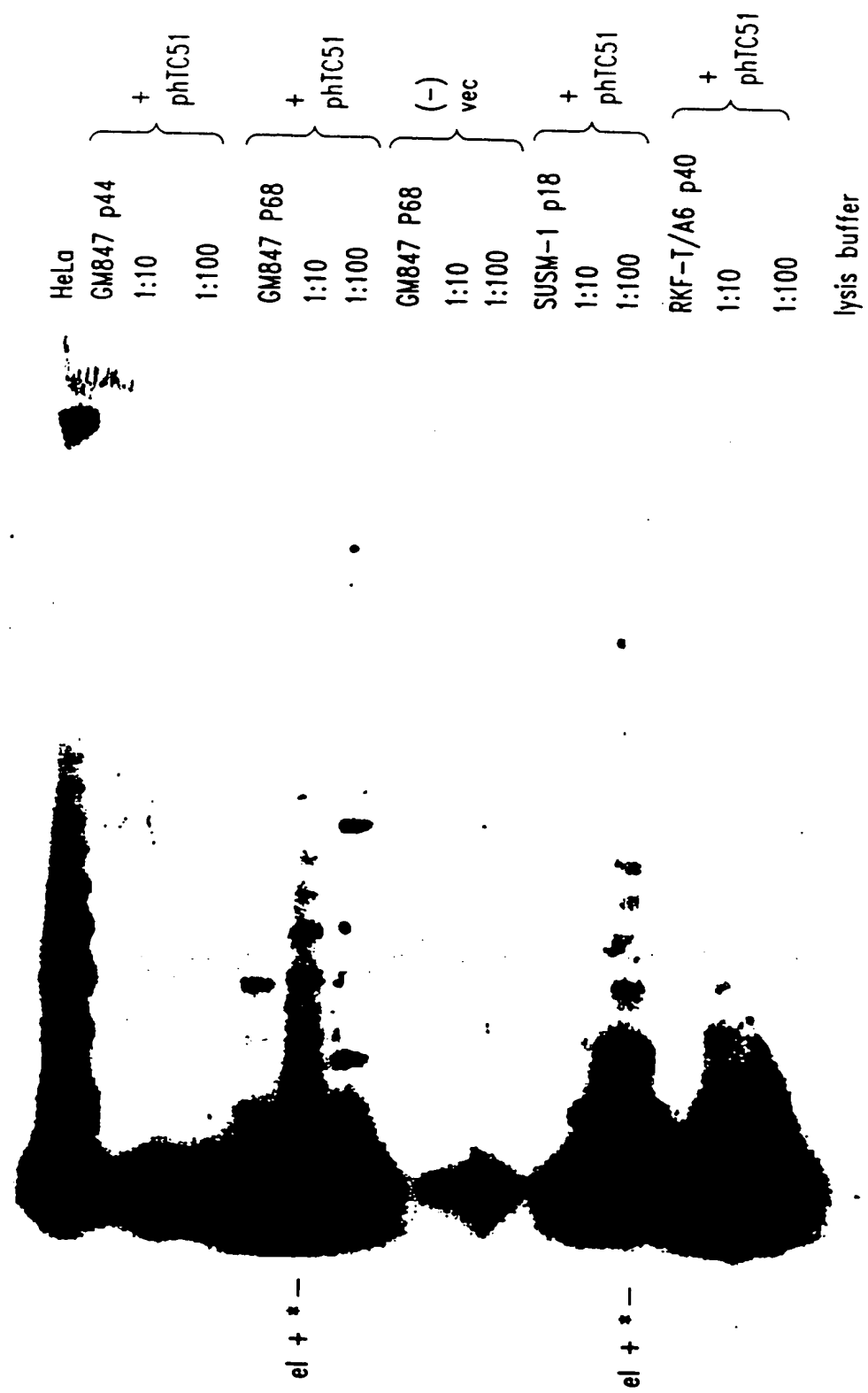


Fig. 12

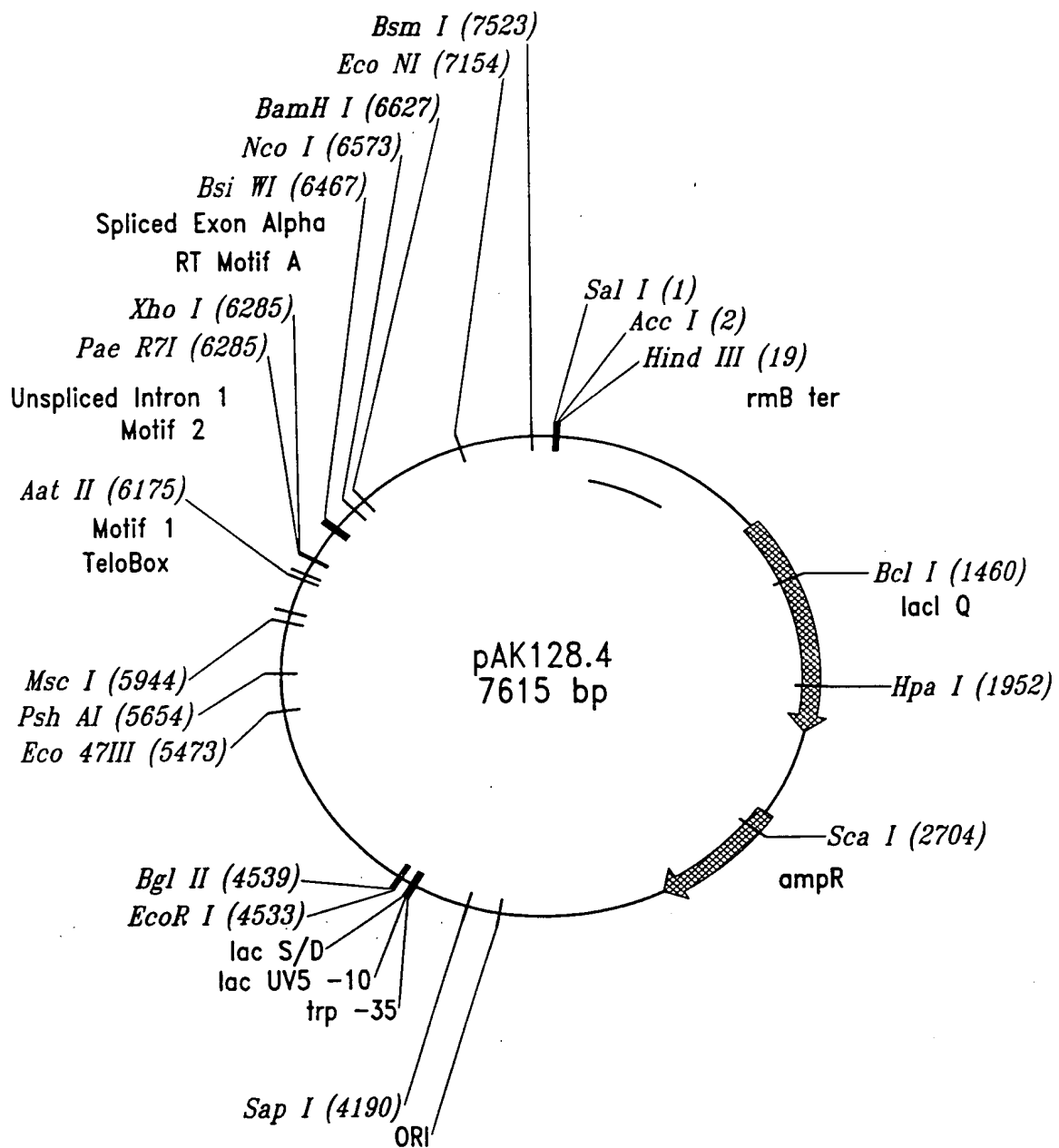


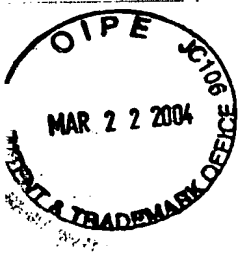
Fig. 13A



LOCUS pAKI28.4 7615 bp dsDNA Circular  
DEFINITION Human telomerase clone with exon beta spliced out

```
1 tgcacctgca ggcatgcaag cttggcactg gccgtcgttt tacaacgtcg tgactgggaa
61 aaccctggcg ttaccaact taatgcctt gcagcacatc cccctttcgc cagctggcgt
121 aatagcgaag aggccgcac cgatcgccct tccaacagt tgcgcagcct gaatggcgaa
181 tggcgcccta tgcggtatit tctccttac catctgtgcg gtatttcaca ccgcataaat
241 tccctgtttt ggcggatgag agaagatttt cagcctgata cagattaaat cagaacgcag
301 aagcggctct ataaaacaga atttgccctg cggcagtagc gcggtgggtc cacctgaccc
361 catgccgaac tcagaagtga aacgccgtag cgccgatggt agtgtggggt ctccccatgc
421 gagagtaggg aactgccagg catcaataa aacgaaaggc tcagtcgaaa gactgggcct
481 ttctgtttat ctgtgtttg tcggtgaacg ctctcctgag taggacaaat ccgccgggag
541 cggatttgaa cgttgcaag caacggcccg gaggggtggc ggcaggacgc ccgccataaa
601 ctgccaggca tcaaattaag cagaaggcca tctgacgga tggccttttt gcgtttctac
661 aaactcttcc tgtcgtcata tctacaagcc atccccccac agatacggta aactagcctc
721 gtttttgcac caggaaagca gggaatttat ggtgcactct cagtacaatc tgctctgatg
781 ccgcatagtt aagccagccc cgacaccgac caacaccgac tgacgcgccc tgacgggctt
841 gtctgtctcc ggcatccgct tacagacaag ctgtgaccgt ctccgggagc tgcattgtgc
901 agaggttttc accgtcatca ccgaaacgcg cgagacgaaa gggcctcgtg atacgcctat
961 ttttataggt taatgtcatg ataataatgg tttcttagac gtgaggttct gtacccgaca
1021 ccatcgaatg gtgcaaaacc tttcgcggtg tggcatgata gcgccgggaa gagagtcaat
1081 tcagggtggt gaattgtgaa ccagtaacgt tatacagatg cgcagagtat gccggtgtct
1141 cttatcagac cgtttccgac gtggtgaacc aggccagcca cgtttctgcg aaaacgcggg
1201 aaaaagtgga agcggcgatg gcggagctga attacattcc caaccgcgtg gcacaacaac
1261 tggcgggcaa acagtcgttg ctgattggcg ttgccacctc cagtctggcc ctgcacgcgc
1321 cgtcgcaaat tgtcgcggcg attaaatctc gcgccgatca actgggtgcc agcgtggtgg
1381 tgtcgatggt agaacgaagc ggcgtcgaag cctgtaaagc ggcggtgcac aatcttctcg
1441 cgcaacgcgt cagtgggctg atcattaact atccgctgga tgaccaggat gccattgctg
1501 tggagctgac ctgcactaat gttccggcgt tatttcttga tgtctctgac cagacacca
1561 tcaacagtat tttttctcc catgaagacg gtacgcgact gggcgtggag catctggtcg
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1681 tgcgtctggc tggctggcat aaatatctca ctcgcaatca aattcagccg atagcggaac
1741 ggaagggcga ctggagtgcc atgtccggtt ttcaacaaac catgcaaatg ctgaatgagg
1801 gcatcgttcc cactgcgatg ctggttgcca acgatcagat ggcgctgggc gcaatgcgcg
1861 ccattaccga gtccgggctg cgcgttggtg cggatatctc ggtagtggga tacgacgata
1921 ccgaagacag ctcatgttat atcccgccgt taaccacat caaacaggat tttcgccctg
1981 tggggcaaac cagcgtggac cgcttgctgc aactctctca gggccaggcg gtgaagggca
2041 atcagctggt gccgctctca ctggtgaaaa gaaaaaccac cctggcgccc aatacgcaaa
2101 ccgcctctcc ccgcgcgttg gccgattcat taatgcagct ggcacgacag gtttcccgac
2161 tggaaagcgg gcagtgagcg caacgcaatt aatgtaagt agctcactca ttaggcaccc
2221 caggctttac actttatgct tccgacctgc aagaacctca cgtcagggtg cacttttcgg
2281 ggaaatgtgc gcggaacccc ttttgttta tttttctaaa tacattcaaa tatgtatccg
2341 ctcatgagac aataaccctg ataaatgctt caataatatt gaaaaaggaa gagtatgagt
2401 attcaacatt tccgtgtcgc cttattccc ttttttgcgg ctttttgcc tctgttttt
2461 gctcaccag aaacgctggt gaaagtaaaa gatgctgaag atcagttggg tgcacgagtg
2521 ggttacatcg agaactggat ctcaacagcg gtaagatcct tgagagtttt cgcgccgaag
2581 aacgttttcc aatgatgagc acttttaaag ttctgctatg tggcgcggtg ttatcccgta
2641 ttgacgccgg gcaagagcaa ctcggtcgcc gcatacacta ttctcagaat gacttggtg
```

*Fig. 13B*



2701 agtactcacc agtcacagaa aagcatctta cggatggcat gacagtaaga gaattatgca  
2761 gtgctgccat aaccatgagt gataacactg cggccaactt acttctgaca acgatcggag  
2821 gaccgaagga gctaaccgct tttttgcaca acatggggga tcatgtaact cgccttgatc  
2881 gttgggaacc ggagctgaat gaagccatac caaacgacga gcgtgacacc acgatgcctg  
2941 tagcaatggc aacaacgttg cgaaactat taactggcga actacttact ctgacttccc  
3001 ggcaacaatt aatagactgg atggaggcgg ataaagtgc aggaccactt ctgcgctcgg  
3061 cccitccggc tggttggttt attgctgata aatctggagc cggtgagcgt gggctctcgg  
3121 gtatcattgc agcactggg ccagatggta agccctccg tatcgtagt atctacacga  
3181 cggggagtcg ggcaactatg gatgaacgaa atagacagat cgctgagata ggtgcctcac  
3241 tgattaagca ttggttaactg tcagaccaag tttactcata tatactttag attgatttaa  
3301 aacttcattt ttaatttaaa aggatctagg tgaagatcct ttttgataat ctcatgacca  
3361 aaatccctta acgtgagttt tcgttccact gagcgtcaga ccccgtagaa aagatcaaaag  
3421 gatcttcttg agatcctttt tttctgcgcg taatctgctg cttgcaaaca aaaaaaccac  
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5461 gcctgccccg gcgtacttg caaatgcggc cctgtttct ggagctgctt gggaaccacg  
5521 cgcagtgcgc ctacggggtg ctctcaaga cgcactgccc gctgcgagct gcggtcacc

Fig. 13C



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5701 tgtacggctt cgtgcgggcc tgctgcgcc ggctgggtgcc cccaggcctc tggggctcca  
5761 ggcacaacga acgccgttc ctcaggaaca ccaagaagt catctccctg ggggaagcatg  
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5881 gcaggagccc aggggttggc tgtgttccgg ccgcagagca ccgtctgctg gaggagatcc  
5941 tggccaagtt cctgcactgg ctgatgagtg tgtacgtcgt cgagctgctc aggtctttct  
6001 tttatgtcac ggagaccacg tttcaaaaga acaggctctt tttctaccgg aagagtgtct  
6061 ggagcaagtt gcaaagcatt ggaatcagac agcacttgaa gaggggtgcag ctgcccggagc  
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6481 cccaggacag gctcacggag gtcacgcca gcatcatcaa accccagaac acgtactgcg  
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6601 gccacgtcct acgtccagtg ccaggggatc ccgcagggt ccactctctc cacgtgtctc  
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7201 cagcaagttt ggaagaaccc cacatttttc ctgcgcgtca tctctgacac ggctccctc  
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7441 tttccccag ggatgtcgt gggggccaag ggcgcgcgg gccctctgcc ctccgaggcc  
7501 gtgcagtggc tgtgccacca agcattcctg ctcaagctga ctcgacaccg tgtcacctac  
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*Fig. 13D*



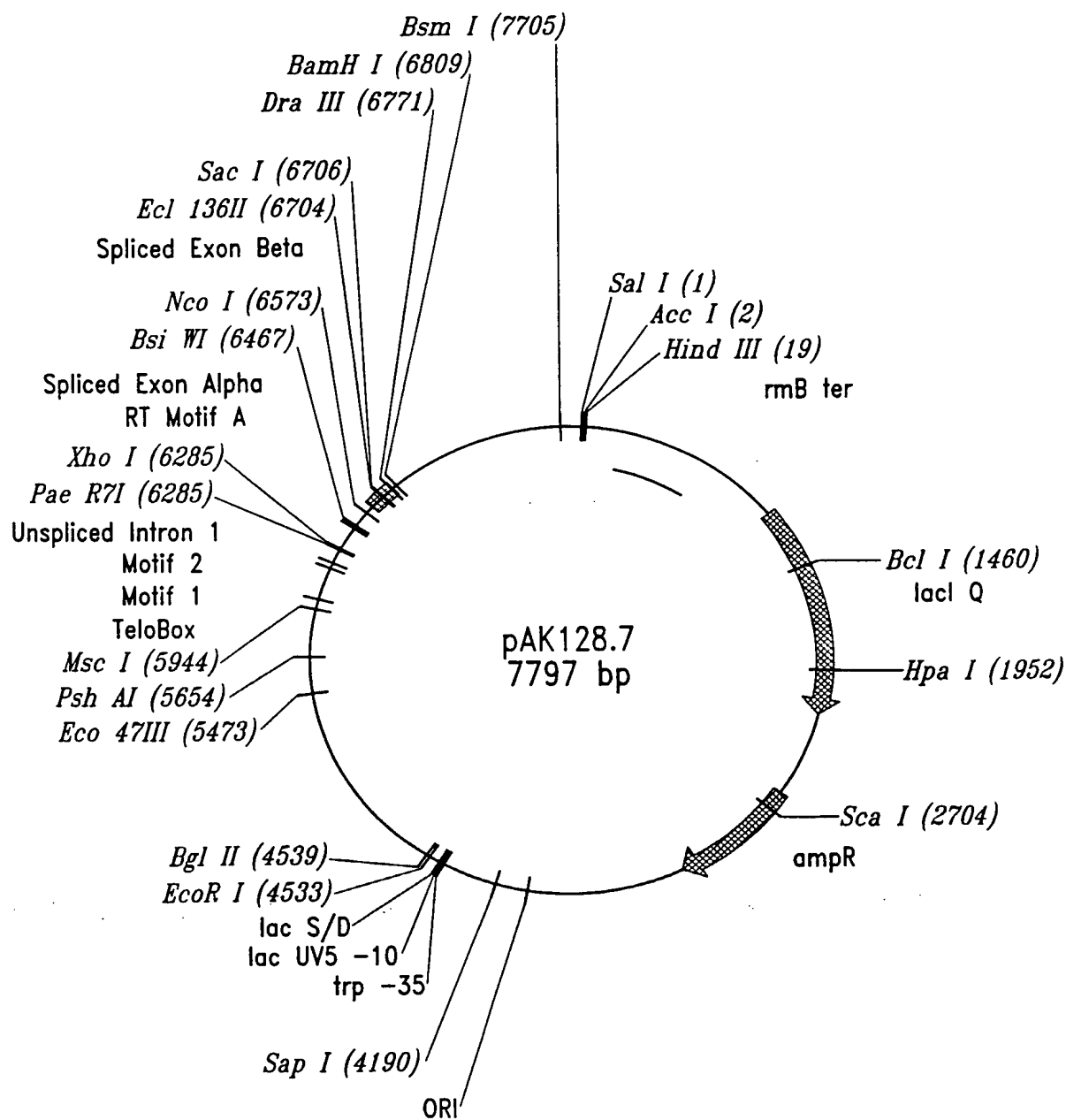


Fig. 14A



LOCUS pAKI28.7 7797 bp dsDNA Circular  
DEFINITION Human telomerase clone with alternative C-terminus

```
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61 aaccctggcg ttacccaact taatcgctt gcagcacatc cccctttcgc cagctggcgt
121 aatagcgaag aggcccgcac cgatcgccct tccaacagt tgcgcagcct gaatggcgaa
181 tggcgctga tgcggtatit tctccttacg catctgtgcg gtatttcaca ccgcataaat
241 tccctgtttt ggcggatgag agaagatit cagcctgata cagattaaat cagaacgcag
301 aagcggctcg ataaaacaga atttgcttg cggcagtagc gcggtggtcc cacctgacct
361 catgccgaac tcagaagtga aacgccgtag cgccgatggt agtgtgggt ctccccatgc
421 gagagtaggg aactgccagg catcaaataa aacgaaaggc tcagtcgaaa gactgggcct
481 ttcgttttat ctgtgtttg tcggtgaacg ctctctgag taggacaaat ccgcccggag
541 cggatttgaa cgttgcaag caacggcccg gaggggtggc ggcaggacgc ccgcataaa
601 ctgccaggca tcaaattaag cagaaggcca tcctgacgga tggcctttt gcgtttctac
661 aaactcttcc tgcgtcata tctacaagcc atccccccac agatacggta aactagcctc
721 gtttttgcag caggaaagca gggaatttat ggtgcactct cagtacaatc tgctctgatg
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1561 tcaacagtat tattttctcc catgaagacg gtacgcgact ggcggtggag catctggctg
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2641 ttgacgccgg gcaagagcaa ctcggtcgcc gcatacacta ttctcagaat gacttgggtg
```

*Fig. 14B*



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2821 gaccgaagga gctaaccgct tttttgcaca acatggggga tcatgtaact cgcttgatc  
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2941 tagcaatggc aacaacgttg cgcaaaactat taactggcga actacttact ctgcttccc  
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3121 gtatcattgc agcactgggg ccagatggta agccctcccg tatcgtagt atctacacga  
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3361 aaatccctta acgtgagttt tcgttccact gagcgtcaga ccccgtagaa aagatcaaag  
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Fig. 14C



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7681 ccgtgcagtg gctgtgccac caagcatttc tgcctaaagt gactcgacac cgtgtcacct  
7741 acgtgccact cctggggtca ctcaggacag gcaagtgtgg gtggaggcca gtgcggg

*Fig. 14D*

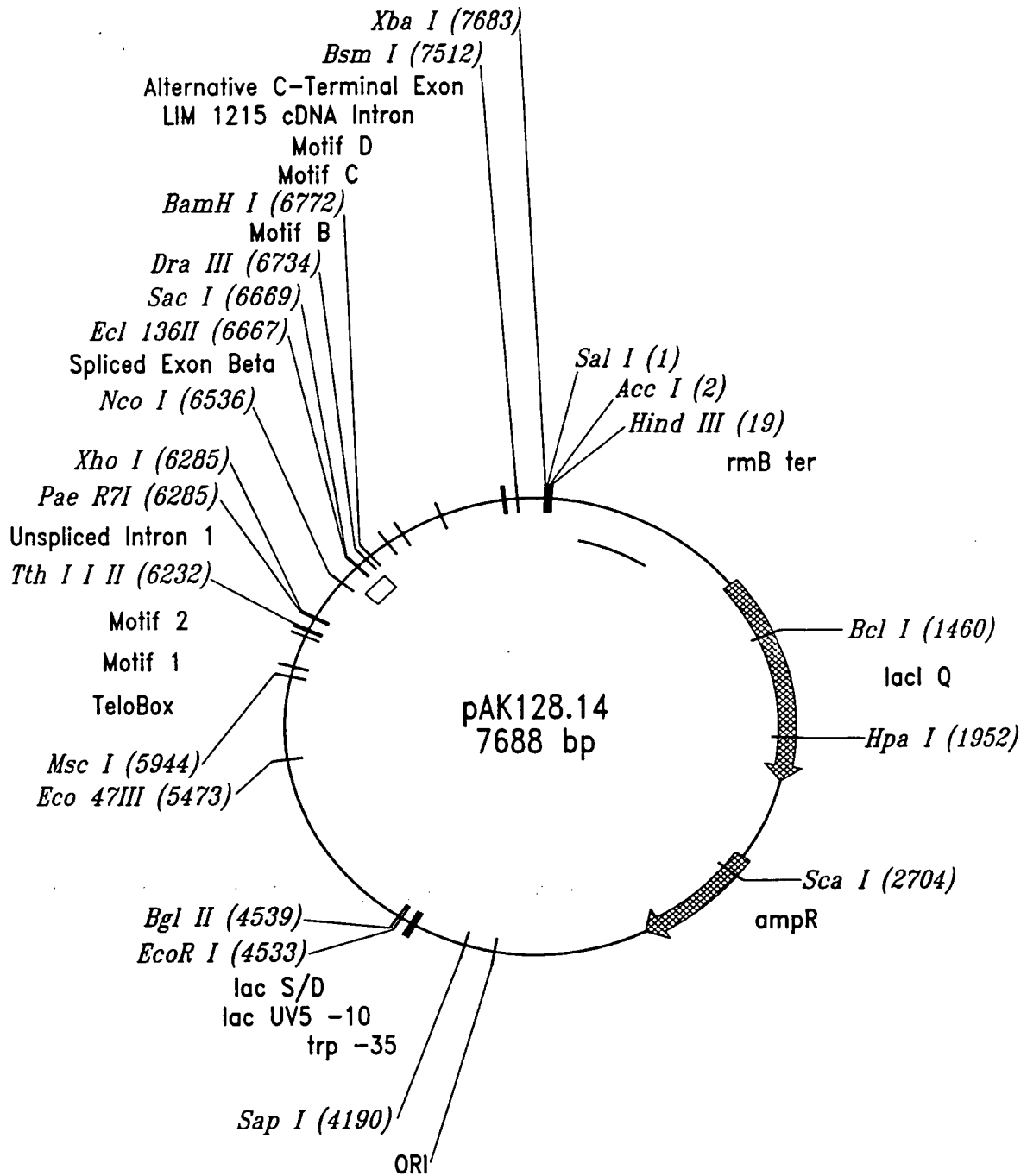


Fig. 15A



LOCUS pAKI28.14 7688 bp dsDNA Circular  
DEFINITION Human telomerase clone with exon alpha spliced out

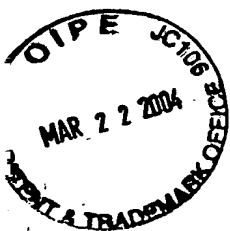
```
1 tcgacctgca ggcattgcaag cttggcactg gccgtcgttt tacaacgtcg tgactgggaa
61 aaccctggcg ttaccaact taatgcctt gcagcacatc cccctttcgc cagctggcgt
121 aatagcgaag aggccgcac cgatcgccct tccaacagt tgcgcagcct gaatggcgaa
181 tggcgctga tgcggtatit tctccttac catctgtgcg gtatttcaca ccgcataaat
241 tccctgtttt ggcggatgag agaagatttt cagcctgata cagattaaat cagaacgcag
301 aagcggctctg ataaaacaga atttgccctg cggcagtagc gcggtgggtc cactgaccc
361 catgccgaac tcagaagtga aacgccgtag cgccgatggt agtgtggggt ctcccatgc
421 gagagtaggg aactgccagg catcaataaa aacgaaaggc tcagtcgaaa gactgggcct
481 ttcgttttat ctgtgtttg tcggtgaacg ctctcctgag taggacaaat ccgccgggag
541 cggatttgaa cgttgcgaag caacggcccg gaggggtggc ggcaggacgc ccgccataaa
601 ctgccaggca tcaaattaag cagaaggcca tctgacgga tggccttttt gcgtttctac
661 aaactcttcc tgtcgtcata tctacaagcc atccccccac agatacggta aactagcctc
721 gtttttgcac caggaaagca gggaaattat ggtgcactct cagtacaatc tgctctgatg
781 ccgcatagtt aagccagccc cgacaccgcg caacaccgcg tgacgcgccc tgacgggctt
841 gtctgtctcc ggcattccgt tacagacaag ctgtgaccgt ctccgggagc tgcattgttc
901 agaggttttc accgtcatca ccgaaacgcg cgagacgaaa gggcctcgtg atacgcctat
961 ttttataggt taatgtcatg ataataatgg tttcttagac gtgaggttct gtaccgcaca
1021 ccatcgaatg gtgcaaaacc tttcgcggta tggcatgata gcgccgggaa gagagtcaat
1081 tcagggtggt gaattgtgaa ccagtaacgt tatacgtatg cgcagagtat gccggtgtct
1141 cttatcagac cgtttcccgc gtggtgaacc aggccagcca cgtttctgcg aaaacgcggg
1201 aaaaagtgga agcggcgatg gcggagctga attacattcc caaccgcgtg gcacaacaac
1261 tggcgggcaa acagtcgttg ctgattggcg ttgccacctc cagtctggcc ctgcacgcgc
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1501 tggaagctgc ctgcactaat gttccggcgt tatttcttga tgtctctgac cagacacca
1561 tcaacagtat tttttctcc catgaagacg gtacgcgact gggcgtggag catctggtcg
1621 cattgggtca ccagcaaatc gcgctgttag cgggcccatt aagtctgtgc tcggcgcgctc
1681 tgcgtctggc tggctggcat aaatatctca ctgcgaatca aattcagccg atagcggaac
1741 gggaaggcga ctggagtgcc atgtccggtt ttcaacaaac catgcaaatg ctgaatgagg
1801 gcatcgttcc cactgcgatg ctggttgcca acgatcagat ggcgctgggc gcaatgcgcg
1861 ccattaccga gtccgggctg cgcttggtg cggatatctc ggtagtggga tacgacgata
1921 ccgaagacag ctcatgttat atcccgccgt taaccacat caaacaggat tttcgctgc
1981 tggggcaaac cagcgtggac cgcttgctgc aactctctca gggccaggcg gtgaagggca
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2221 caggctttac actttatgct tccgacctgc aagaacctca cgtcagggtg cacttttcgg
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2401 attcaacatt tccgtgtcgc cttattccc tttttgcgg cattttgcct tcctgtttt
2461 gctcaccag aaacgctggt gaaagtaaaa gatgtgaag atcagttggg tgcacgagtg
2521 ggttacatcg agaactgat ctcaacagcg gtaagatcct tgagagtttt cggccgaag
2581 aacgttttcc aatgatgagc acttttaaa ttctgctatg tggcgcggtt ttatcccgta
2641 ttgacgcccg gcaagagcaa ctcggtcgcc gcatacacta ttctcagaat gacttggttg
```

*Fig. 15B*



2701 agtactcacc agtcacagaa aagcatctta cggatggcat gacagtaaga gaattatgca  
2761 gtgctgccat aaccatgagt gataacactg cggccaactt acttctgaca acgatcggag  
2821 gaccgaagga gctaaccgct tttttgcaca acatggggga tcatgtaact cgccttgatc  
2881 gttgggaacc ggagctgaat gaagccatac caaacgacga gcgtgacacc acgatgcctg  
2941 tagcaatggc aacaacgttg cgcaaaactat taactggcga actacttact cttagcttccc  
3001 ggcaacaatt aatagactgg atggaggcgg ataaagtgtc aggaccactt ctgcgctcgg  
3061 cccttccggc tggctggttt attgctgata aatctggagc cggtgagcgt gggctctcgcg  
3121 gtatcattgc agcactgggg ccagatggta agccctcccg tatcgtagt tcttacacga  
3181 cggggagtcg ggcaactatg gatgaacgaa atagacagat cgtgagata ggtgcctcac  
3241 tgattaagca ttggttaactg tcagaccaag ttactcata tatactttag attgatttaa  
3301 aacttcattt ttaatttaaa aggatctagg tgaagatcct ttttgataat ctcatgacca  
3361 aaatccctta acgtgagttt tcgttccact gagcgtcaga ccccgtagaa aagatcaaag  
3421 gatcttcttg agatcctttt tttctgcgcg taatctgctg cttgcaaaca aaaaaaccac  
3481 cgctaccagc ggtggtttgt ttgccggatc aagagctacc aactctttt ccgaaggtaa  
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3601 accacttcaa gaactctgta gcaccgccta catacctcgc tctgctaate ctgttaccag  
3661 tggtctgtgc cagtggcgat aagtcgtgtc ttaccgggtt ggactcaaga cgatagttac  
3721 cggataaggc gcagcggtcg ggctgaacgg ggggttcgtg cacacagccc agcttggagc  
3781 gaacgaccta caccgaactg agatacctac agcgtgagca ttgagaaagc gccacgcttc  
3841 ccgaagggag aaaggcggac aggtatccgg taagcggcag ggtcggaca ggagagcgca  
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5401 tggagaccat ctttctgggt tccaggccct ggatgccagg gactccccgc aggttgcccc  
5461 gcctgccccg gcgtacttg caaatgcggc cctgtttct ggagctgctt gggaaccacg  
5521 cgcagtgcc ctacgggggtg ctctcaaga cgcactgccc gctgcgagct gcggtcacc

Fig. 15C



5581 cagcagccgg tgtctgtgcc cgggagaagc cccagggctc tgtggcggcc cccgaggagg  
5641 aggacacaga cccccgtcgc ctggtgcagc tgctccgcca gcacagcagc ccctggcagg  
5701 tgtacggctt cgtgcgggcc tgccctgcgc ggctgggtgcc cccaggcctc tggggctcca  
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7681 atctagag

*Fig. 15D*